SEQUENCE LISTING

<110> ASAHI KASEI KABUSHIKI KAISHA

<120> NF-κB Activating Gene

<130> F101131-US

<150> JP 2000-402288
<151> 2000-12-28

<150> JP 2001-088912
<151> 2001-03-26

<150> JP 2001-254018
<151> 2001-08-24

<150> US 60/258,315
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<151> 2001-08-24

<160> 182

<170> PatentIn Ver. 2.0

<210> 1

<211> 167

<212> PRT

<213> Homo sapiens

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Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val
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Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr
                20   25   30

Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser
                35   40   45

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
                50   55   60

Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
65   70   75   80

Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
                85   90   95

Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr
                100   105   110

Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
                                2/735

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            115                   120                   125
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Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser

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            130                   135                   140
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Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly

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      145                   150                   155                   160
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Tyr Gly Gly Thr Arg Arg Arg

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                  165
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<210> 2

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (194)..(694)

<400> 2

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gtctggaaag cagcacggct ttgcctcttt ctctgattat tattataagt ggtcctcggc 180

ggattcctgt aac atg agt gga ttg att acc atc gtg gta ctc ctt ggg 229

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                  Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly
                   1               5                   10


atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct    277
Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser
         15                  20                  25


cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga    325
Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg
         30                  35                  40


ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc    373
Phe Thr Asn Ser Ala Gly Pro Pro Pro Gly Phe Lys Ser Glu Phe
45                  50                  55                  60


aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt    421
Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser
                   65                  70                  75


gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg    469
Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp
         80                  85                  90


aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat    517
Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn
         95                  100                 105


aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct    565
Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro
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                 110                    115                    120


     ccc tcc tac cct ggc acg tgg aat agg gct tac tca ccc ctt cat gga   613
     Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
     125                    130                    135                    140


     ggc tcg ggc agc tat tcg gta tgt tca aac tca gac acg aaa acc aga   661
     Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg
                      145                    150                    155


     act gca tca gga tat ggt ggt acc agg aga cga taaagtagaa agttggagtc 714
     Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
                 160                    165



     aaacactgga tgcagaaatt ttggattttt catcactttc tctttagaaa aaaagtacta 774


     cctgttaaca attgggaaaa ggggatattc aaaagttcgg tggtgttatg tccagtgtag 834


     ctttttgtat tctattattt gaggctaaaa gttgatgtgt gacaaaatac ttatgtgttg 894
                                              .

     tatgtcagtg taacatgcag atgtatattg cagtttttga aagtgatcat tactgtggaa 954


     tgctaaaaat acattaattt ctaaaacctg tgatgcccta agaagcatta agaatgaagg 1014


     tgttgtacta atagaaacta agtacagaaa atttcagttt taggtggttg tagctgatga 1074


     gttattacct catagagact gtaatattct atttggtatt atattatttg atgtttgctg 1134


     ttcttcaaac atttaaatca agctttggac taattatgct aatttgtgag ttctgatcac 1194
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<210> 3

<211> 339

<212> PRT

<213> Homo sapiens

<400> 3

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            20   25   30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
            35   40   45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
        50   55   60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65   70   75   80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
                85   90   95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
                100   105   110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
                115   120   125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
                130   135   140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145   150   155   160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
                165   170   175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
                180   185   190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
                195   200   205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
                7/735

                210   215   220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225   230   235   240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
                    245   250   255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
                    260   265   270

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
                    275   280   285

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
                    290   295   300

Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
305   310   315   320

Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
                    325   330   335

Arg Arg Arg

<210> 4

<211> 1924

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115)..(1131)

<400> 4

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                                                                    Met

                                                                  1

gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc   165
Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly
                  5   10   15

ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac   213
Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
             20   25   30

cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat   261
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
             35   40   45

gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa   309
Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
50   55   60   65

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tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata    357
Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
                70                  75                  80


cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt    405
Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
                85                  90                  95


aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc    453
Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
                100                 105                 110


tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct    501
Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
                115                 120                 125


tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa    549
Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
130                 135                 140                 145


ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat    597
Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
                150                 155                 160


tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att    645
Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
                165                 170                 175
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acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc      693
Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
        180                 185                 190


ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca      741
Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
        195                 200                 205


ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc      789
Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
210                 215                 220                 225


cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt      837
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
                230                 235                 240


gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa      885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
                245                 250                 255


aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta      933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu
                260                 265                 270


gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg      981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
        275                 280                 285


tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg     1029
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Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
290   295   300   305

gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca   1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
                        310   315   320

aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg   1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
                325   330   335

aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt   1181
Arg Arg

catcactttc tctttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc   1241

aaaagttcgg tggtgttatg tccagtgtag ctttttgtat tctattattt gaggctaaaa   1301

gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattg   1361

cagtttttga aagtgatcat tactgtggaa tgctaaaaat acattaattt ctaaaacctg   1421

tgatgcccta agaagcatta agaatgaagg tgttgtacta atagaaacta agtacagaaa   1481

atttcagttt taggtggttg tagctgatga gttattacct catagagact gtaatattct   1541

atttggtatt atattatttg atgtttgctg ttcttcaaac atttaaatca agctttggac   1601

taattatgct aatttgtgag ttctgatcac ttttgagctc tgaagctttg aatcattcag   1661
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tggtggagat ggccttctgg taactgaata ttaccttctg taggaaaagg tggaaaataa 1721

gcatctagaa ggttgttgtg aatgactctg tgctggcaaa aatgcttgaa acctctatat 1781

ttctttcgtt cataagaggt aaaggtcaaa tttttcaaca aaagtctttt aataacaaaa 1841

gcatgcagtt ctctgtgaaa tctcaaatat tgttgtaata gtctgtttca atcttaaaaa 1901

gaatcaataa aaacaaacaa ggg   1924

<210> 5
<211> 127
<212> PRT
<213> Homo sapiens

<400> 5

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
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Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
                20   25   30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
            35   40   45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
        50   55   60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala

  65   70   75   80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile

         85   90   95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe

     100   105   110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser

     115   120   125

<210> 6

<211> 702

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(605)

<400> 6

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ggcgtcttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa ggggggcgc aaaa atg gct ggg gca   236
                                                          Met Ala Gly Ala
                                                        1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att   284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
 5   10   15   20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct   332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
               25   30   35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat   380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
             40   45   50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc   428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
          55   60   65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa   476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
        70   75   80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac   524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
85   90   95   100

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atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg      572
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
                105                 110                 115


gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctcctctcat 625
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
                120                 125


ccctttcttc cctttgagca ttgccctctt tgggttcttt ttgagccaat tctaataaaa 685


gtaaaaatgg taatagt                                                  702
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<210> 7

<211> 233

<212> PRT

<213> Homo sapiens

<400> 7

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Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
                20                  25                  30


Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
                35                  40                  45


Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
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50   55   60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65   70   75   80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
                  85   90   95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
                  100   105   110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu
                  115   120   125

Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala
          130   135   140

Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu
145   150   155   160

Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr
                  165   170   175

Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly
                  180   185   190

Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser
          195   200   205

Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr
        210   215   220

Pro Ser Gly Met Val Phe His Arg Val
225   230

<210> 8

<211> 2409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(923)

<400> 8

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa ggggggggcgc aaaa atg gct ggg gca 236
                                                  Met Ala Gly Ala
                                                    1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att   284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

| | 5 | | | | 10 | | | | 15 | | | | 20 | | |

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ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct    332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
                25                  30                  35


cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat    380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
                40                  45                  50


gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc    428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
                55                  60                  65


aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa    476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
        70                  75                  80


att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac    524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
85                  90                  95                  100


atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg    572
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
                105                 110                 115


gac att gcc ttc aag cta aac aac caa atc aga gaa aat gca gaa gtc    620
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val
        120                 125                 130
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tcc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg    668
Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp
        135             140             145


act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc    716
Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe
        150             155             160


aca tct ccc aag act cca gag cat gag ggc cgt tac tat gaa tgt gat    764
Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp
165             170             175             180


gtc ctt cct tac gcc cag cat ctt cat cat tat ggt gtg gta ttg gag    812
Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu
                185             190             195


gag gat cac cat gat gtc ccg acc ccc agt gct tct gga aaa agt cat    860
Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His
                200             205             210


ctt tgc cct tgg gat ttc cat gac ctt tat caa tat ccc agt gga atg    908
Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met
        215             220             225


gtt ttc cat cgg gtt tgactggacc tggatgctgc tgtttggtga catccgacag    963
Val Phe His Arg Val
        230
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ggcatcttct atgcgatgct tctgtccttc tggatcatct tctgtggcga gcacatgatg 1023

gatcagcacg agcggaacca catcgcaggg tattggaagc aagtcggacc cattgccgtt 1083

ggctccttct gcctcttcat atttgacatg tgtgagagag gggtacaact cacgaatccc 1143

ttctacagta tctggactac agacattgga acagagctgg ccatggcctt catcatcgtg 1203

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gtctttgctc tgatgttctt gtatgcacca tcccataaaa actatggaga agaccagtcc 1563

aatggcgatc tgggtgtcca tagtggggaa gaactccagc tcaccaccac tatcacccat 1623

gtggacggac ccactgagat ctacaagttg acccgcaagg aggcccagga gtaggaggct 1683

gcagcgcccg gctgggacgg tctctccata ccccagcccc tctaactaga gtggggagca 1743

tgccagagag agctcaatgt acaaatgaat gcctcatggc tcttagctgt ggtttcttgg 1803

accagcggca tggacatttg tcagtttgcc ttctgacggt agcttttgga ggaagattcc 1863

tgcagccact aatgcattgt gtatgataac aaaaactctg gtatgacaca ttttctgtga 1923

tcattgttaa ttagtgacat agtaacatct gtagcagctg gttagtaaac ctcatgtggg 1983

ggtggggtgg gggtgtattc cttgggggat ggtttgggcc gaatggggag tggaatattt 2043

gacatttttc ctgttttaaa ttctaggata gattttaaca tcctttgcgg tcccagtcca 2103

aggtaggctg gtgtcatagt cttctcactc ctaatccatg accactgttt ttttcctatt 2163

tatatcacca ggtagcccac tgagttaata tttaagttgt caatagataa gtgtccctgt 2223

tttgtggcat aatataactg aatttcatga gaagatttat tccaccaggg gtatttcagc 2283

tttgaaacca aatctgtgta tctaatacta accaatctgt tggatgtggg ttttaaaaaa 2343

tgtttgctaa actacccaag taagatttac tgtattaaat ggccttcggg tctgaaaagc 2403

tttttt 2409

<210> 9

<211> 198

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu Ser

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     1                 5                  10                 15

   Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp
                 20                 25                 30

   Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
                 35                 40                 45

   Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
                 50                 55                 60

   Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
   65                 70                 75                 80

   Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
                 85                 90                 95

   Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu
                 100                105                110

   Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile
                 115                120                125

   Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp
                 130                135                140

   Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala
   145                150                155                160
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Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln
                165   170   175

Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp
                180   185   190

Arg His Val Val Leu Ser
            195

<210> 10

<211> 1498

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86)..(679)

<400> 10

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ctgtgggacc gctgggcccc cagcg atg gcg acc ctg tgg gga ggc ctt ctt 112
                              Met Ala Thr Leu Trp Gly Gly Leu Leu
                               1   5

cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160
Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu
 10   15   20   25

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ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga   208
Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg
              30   35   40

tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat   256
Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr
              45   50   55

aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag   304
Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu
              60   65   70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt   352
Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys
              75   80   85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att   400
Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
90   95   100   105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat   448
Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr
             110   115   120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca   496
Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala
             125   130   135

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cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca      544
Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala
        140             145                 150


aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg      592
Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu
        155             160                 165


aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag      640
Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu
170             175                 180                 185


cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa      689
Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser
                190                 195


ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggtttt 749


gctgggtttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaact 809


ggaagcaaaa acttgcttga tttttttttc ttgttaacgt aataatagag acattttaa 869


aagcacacag ctcaaagtca gccaataagt cttttcctat ttgtgacttt tactaataaa 929


aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctcttttc 989


accacatagt tttaacttga ctttcaagat aattttcagg gttttttgttg ttgttgtttt 1049


ttgtttgttt gttttggtgg gagaggggag ggatgcctgg gaagtggtta acaactttttt 1109
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tcaagtcact ttactaaaca aacttttgta aatagacctt accttctatt ttcgagtttc 1169

atttatattt tgcagtgtag ccagcctcat caaagagctg acttactcat ttgacttttg 1229

cactgactgt attatctggg tatctgctgt gtctgcactt catggtaaac gggatctaaa 1289

atgcctggtg gcttttcaca aaaagcagat tttcttcatg tactgtgatg tctgatgcaa 1349

tgcatcctag aacaaactgg ccatttgcta gtttactcta aagactaaac atagtcttgg 1409

tgtgtgtggt cttactcatc ttctagtacc tttaaggaca aatcctaagg acttggacac 1469

ttgcaataaa gaaattttat tttaaaccc 1498

<210> 11

<211> 221

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly
1   5   10   15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu
                20   25   30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

```
              35                        40                        45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro
      50                        55                        60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu
      65                        70                        75                        80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu
                        85                        90                        95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile
                        100                       105                       110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe
                        115                       120                       125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala
                        130                       135                       140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp
145                       150                       155                       160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly
                        165                       170                       175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe
                        180                       185                       190
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Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr
     195   200   205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr
     210   215   220

<210> 12

<211> 1864

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(815)

<400> 12

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cccctcggcc tcccagcgct cccaagccgc agcggccgcg ccccttcagc tagctcgctc 120

gctcgctctg cttccctgct gccggctgcg cc atg gcg ttg gcg ttg gcg gcg 173
                                          Met Ala Leu Ala Leu Ala Ala
                                          1   5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221
Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln
     10   15   20

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aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct      269
Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro
        25              30              35


cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac      317
Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr
 40              45              50              55


aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca      365
Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr
                60              65              70


aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act      413
Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr
            75              80              85


atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat      461
Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp
            90              95              100


ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg      509
Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met
        105             110             115


tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg      557
Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu
120             125             130             135


tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca      605
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Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser
            140   145   150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc   653
Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser
            155   160   165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg   701
Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
            170   175   180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat   749
Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
            185   190   195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc   797
Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
200   205   210   215

aga gtt ctc ttt att tat taaagatgtt ttctggcaaa ggccttcctg   845
Arg Val Leu Phe Ile Tyr
            220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtgaa tcaagatgca 905

gaacacagag gaataatcac ctgctttaaa aaaataaagt actgttgaaa agatcatttc 965

tctctatttg ttcctaggtg taaaatttta atagttaatg cagaattctg taatcattga 1025

atcattagtg gttaatgttt gaaaaagctc ttgcaatcaa gtctgtgatg tattaataat 1085

gccttatata ttgtttgtag tcattttaag tagcatgagc catgtccctg tagtcggtag 1145

ggggcagtct tgctttattc atcctccatc tcaaaatgaa cttggaatta aatattgtaa 1205

gatatgtata atgctggcca ttttaaaggg gttttctcaa aagttaaact tttgctatga 1265

ctgtgttttt gcacataatc catatttgct gttcaagtta atctagaaat ttattcaatt 1325

ctgtatgaac acctggaagc aaaatcatag tgcaaaaata catttaaggt gtggtcaaaa 1385

ataagtcttt aattggtaaa taataagcat taattttta tagcctgtat tcacaattct 1445

gcggtacctt attgtaccta agggattcta aaggtgttgt cactgtataa aacagaaagc 1505

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ttaggccaaa gtctgggagt aaggagagga ttaggtactt aggagcaaag aaagaagtag 1685

cttggaactt ttgagatgat ccctaacata ctgtactact tgcttttaca atgtgttagc 1745

agaaaccagt gggttataat gtagaatgat gtgctttctg cccaagtggt aattcatctt 1805

ggtttgctat gttaaaactg taaatacaac agaacattaa taaatatctc ttgtgtagc 1864

<210> 13

<211> 242

<212> PRT

<213> Homo sapiens

<400> 13

Met	Asp	His	His	Gln	Pro	Gly	Thr	Gly	Arg	Tyr	Gln	Val	Leu	Leu	Asn
1				5					10					15	

Glu	Glu	Asp	Asn	Ser	Glu	Ser	Ser	Ala	Ile	Glu	Gln	Pro	Pro	Thr	Ser
			20					25					30		

Asn	Pro	Ala	Pro	Gln	Ile	Val	Gln	Ala	Ala	Ser	Ser	Ala	Pro	Ala	Leu
			35				40					45			

Glu	Thr	Asp	Ser	Ser	Pro	Pro	Pro	Tyr	Ser	Ser	Ile	Thr	Val	Glu	Val
			50				55					60			

Pro	Thr	Thr	Ser	Asp	Thr	Glu	Val	Tyr	Gly	Glu	Phe	Tyr	Pro	Val	Pro
65					70					75					80

Pro	Pro	Tyr	Ser	Val	Ala	Thr	Ser	Leu	Pro	Thr	Tyr	Asp	Glu	Ala	Glu
				85					90					95	

Lys	Ala	Lys	Ala	Ala	Ala	Met	Ala	Ala	Ala	Ala	Glu	Thr	Ser	Gln	
			100					105					110		

Arg	Ile	Gln	Glu	Glu	Glu	Cys	Pro	Pro	Arg	Asp	Asp	Phe	Ser	Asp	Ala
			115					120					125		

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
        130   135   140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145   150   155   160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
                165   170   175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
            180   185   190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
            195   200   205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
    210   215   220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225   230   235   ·   240

Leu Leu

<210> 14

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(738)

<400> 14

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           Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val
            1               5                   10


ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca    99
Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
     15              20                  25


cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca    147
Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala
 30              35                  40                  45


cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act    195
Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
             50                  55                  60


gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat    243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
             65                  70                  75


ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat    291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
```

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              80                    85                    90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa    339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu
        95                   100                   105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc    387
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
110                   115                   120                   125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg    435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
                  130                   135                   140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc    483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
                  145                   150                   155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga    531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
        160                   165                   170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat    579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
        175                   180                   185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt    627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
190                   195                   200                   205
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ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta    675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
                210               215               220


aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg    723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
                225               230               235


tat ttc ttc tta ttg tagagactgc atcaacccga cattcctttc ttataccaat    778
Tyr Phe Phe Leu Leu
        240
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gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa 838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta 898

caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca catatgcata 958

tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag 1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa 1138

ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac 1198

atgaaacatc ttttgttata tagggtgtat tgaaacctgc agtgctgatt attagaaagg 1258

atttgtcaga tttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa 1318

taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattta gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

ggacatacta gttttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618

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tcaaagttaa ttttctaaat aagataattc tcatttgtgt ttgtctttta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

tctgtttttc ctttcggtta tatctttggt tttgaatacc aacatttaaa atgatggtat 2098

tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158

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catttccaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278

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<210> 15

<211> 242

<212> PRT

<213> Homo sapiens

<400> 15

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
 1   5   10   15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
                20   25   30

Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu
            35   40   45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
        50   55   60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
65   70   75   80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
            85   90   95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln
            100   105   110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
            115   120   125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
            130   135   140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145   150   155   160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
                        165   170   175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
                        180   185   190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
                        195   200   205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
            210   215   220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225   230   235   240

40/735

Leu Leu

<210> 16

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(738)

<400> 16

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　　　　　　　　Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

　　　　　　　　　1　　　　　　　　　　5　　　　　　　　　　　10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

　　　15　　　　　　　　　20　　　　　　　　　25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala

　30　　　　　　　　35　　　　　　　　40　　　　　　　　45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

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                50                        55                        60


gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat      243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
             65                        70                        75


ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat      291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
             80                        85                        90


gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa      339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu
          95                       100                       105


aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc      387
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
110                      115                       120                       125


agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg      435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
             130                       135                       140


gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc      483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
             145                       150                       155


ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga      531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
             160                       165                       170
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ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat     579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
    175               180               185


tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt     627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
190               195               200               205


ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta     675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
              210               215               220


aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg     723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
              225               230               235


tat ttc ttc tta ttg tagagactgc atcaacccga cattcctttc ttataccaat     778
Tyr Phe Phe Leu Leu
        240


gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa     838


gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta     898


caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca catatgcata     958


tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag     1018
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tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag 1078

tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa 1138

ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac 1198

atgaaacatc ttttgttata tagggtgtat tgaaacctgc agtgctgatt attagaaagg 1258

atttgtcaga tttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa 1318

taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattta gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

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aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

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aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

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<210> 17

<211> 336

<212> PRT

<213> Homo sapiens

<400> 17

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met
1   5   10   15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr
            20   25   30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

                    35   40   45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
        50   55   60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
        65   70   75   80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
                    85   90   95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
                    100   105   110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
                    115   120   125

Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr
        130   135   140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145   150   155   160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
                    165   170   175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
                    180   185   190

Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
        195   200   205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
        210   215   220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225   230   235   240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
                245   250   255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
                260   265   270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
                275   280   285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
        290   295   300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305   310   315   320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
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<210> 18

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(1060)

<400> 18

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                                                                  1



cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat       106
Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
            5                   10                  15


agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg       154
Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
        20                  25                  30


gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg       202
Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
 35                  40                  45                  50


ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg       250
Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
                55                  60                  65
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acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac   298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
             70              75              80


tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac   346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
             85              90              95


cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac   394
Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
         100             105             110


tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg   442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
115             120             125             130


cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct   490
Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
             135             140             145


tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca   538
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
             150             155             160


gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc   586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
             165             170             175


gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct   634
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Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
        180             185             190


gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag     682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
195             200             205             210


gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga     730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
            215             220             225


gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att     778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
                230             235             240


ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata     826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
                245             250             255


gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa     874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
                260             265             270


tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat     922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275             280             285             290


gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt     970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu
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●

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                   295                    300                    305


ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa      1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
              310                    315                    320


agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg              1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
              325                    330                    335


tagagactgc atcaacccga cattcctttc ttataccaat gtgaaatttc cagatcatct    1120


gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag    1180


acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc    1240


tttaagtatc tatatttcat ttgttttgca catatgcata tgtgcccatt taagatattt    1300


gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat    1360


cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaatgcc    1420


attgacttct gacctgacat ttagtataat aaaaatgaaa ttcttaacca tgtcaaatga    1480


tttagtttct ggctcttaga ctcatctggc agttctacac atgaaacatc ttttgttata    1540


taaggtgtat tgaaacctgc agtgctgatt attagaaagg atttgtcaga tttttgaaca    1600


tgatatttac attattattt aggaaaactc ttcctgtaaa taaccatgca taacttactt    1660
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tctgcaatgt tttcttagaa attgtgtcca gatagctttc actaatttta aattaagtga 1720

actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatattta 1780

gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa ttttaagaaa atgtgggaat 1840

accaaatgtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900

ttttcagatg ggaagctgca tttttaggat tgcccatctt aagagatctt gcaggaagag 1960

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aagataattc tcatttgtgt ttgtctttta aaaggccaat aaaatatctt tcagtatcat 2080

tgtaataatt ttttagagtt taatttgtaa agcttagcaa ataaaatctt gtactatgaa 2140

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tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg gcatatagga ctgtggggtc 2260

tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320

actactatat ttcccatctt gcaaatcatt ttatgtctca tctgtttttc ctttcggtta 2380

tatctttggt tttgaatacc aacatttaaa atgatggtat tttatctttt aaacttaaaa 2440

attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500

actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaatt 2560

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acagttttgt tttgct   2636

<210> 19

<211> 336

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met
1   5   10   15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr
                20   25   30

Asn Ala Glu Val Ser Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
        35   40   45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
    50   55   60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65   70   75   80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp

                    85   90   95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
            100   105   110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
            115   120   125

Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr
            130   135   140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145   150   155   160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
            165   170   175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
            180   185   190

Lys Ala Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
            195   200   205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
            210   215   220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225   230   235   240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
                245   250   255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
                260   265   270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
                275   280   285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
                290   295   300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305   310   315   320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
                325   330   335

<210> 20

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(1060)

<400> 20

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                                                                Met Ala
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cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat   106
Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
         5   10   15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg   154
Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
        20   25   30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg   202
Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
 35   40   45   50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg   250
Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
                55   60   65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac   298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
                70   75   80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac   346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
                85   90   95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac   394

Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
    100   105   110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg   442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
115   120   125   130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct   490
Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
                135   140   145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca   538
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
                150   155   160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc   586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
                165   170   175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct   634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
    180   185   190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag   682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
195   200   205   210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga   730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
                        57/735

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                215                   220                   225


gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att    778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
            230                   235                   240


ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata    826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
            245                   250                   255


gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa    874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
            260                   265                   270


tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat    922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275                   280                   285                   290


gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt    970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu
            295                   300                   305


ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa    1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
            310                   315                   320


agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg    1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
            325                   330                   335
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tagagactgc atcaacccga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

tttaagtatc tatatttcat ttgttttgca catatgcata tgtgcccatt aagatatt 1300

gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaatgcc 1420

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tgatatttac attattattt aggaaaactc ttcctgtaaa taaccatgca taacttactt 1660

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actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatattta 1780

gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa ttttaagaaa atgtgggaat 1840

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tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320

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actactaaaa ggtacatcta actattcagg gacattttttc catttccaaa aaataaaatt 2560

tattatgctt tataacctct tctgtatttt ctaattttttt cattgtcttt gataaataaa 2620

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<210> 21

<211> 76

<212> PRT

<213> Homo sapiens

<400> 21

Met Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr
1   5   10   15

Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val
            20   25   30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn
            35   40   45

Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr
        50   55   60

Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
65   70   75

<210> 22

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (176)..(403)

<400> 22

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cggcctccgc ggtgcctgcc ttcgctctca ggttgaggag ctcaagcttg ggaaa atg 178
                                                              Met
                                                               1


gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa   226
Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys
              5                   10                  15


aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt   274
Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser
         20                  25                  30


cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa   322
Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys
         35                  40                  45


ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa   370
Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys
50                  55                  60                  65


gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttcctaaagg 423
Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
                 70                  75
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accccatcat ttaaaaaatg gacctgataa tatgaagcat cttccttgta attgtctctg 483

acctttttat ctgagaccgg aattcaggat aggagtctag atatttacct gatactaatc 543

aggaaatata tgatatccgt atttaaaatg tagttagtta tatttaatga cctcattcct 603

aagttccttt ttcgttaatg tagctttcat ttctgttatt gctgtttgaa taatatgatt 663

aaatagaagg tttgtgccag tagacattat gttactaaat cagcacttta aaatctttgg 723

ttctctaatt catatgaatt tgctgtttgc tctaatttct ttgggctctt ctaatttgag 783

tggagtacaa ttttgttgtg aaacagtcca gtgaaactgt gcagggaaat gaaggtagaa 843

ttttgggagg taataatgat gtgaaacata aagatttaat aattactgtc caacacagtg 903

gagcagcttg tccacaaata tagtaattac tatttattgc tctaaggaag attaaaaaaa 963

gatagggaaa agggggaaac ttctttgaaa aatgaaacat ctgttacatt aatgtctaat 1023

tataaaattt taatccttac tgcatttctt ctgttcctac aaatgtatta aacattcagt 1083

tt 1085

<210> 23

<211> 84

<212> PRT

<213> Homo sapiens

<400> 23

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
1   5   10   15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
                20   25   30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
                35   40   45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
            50   55   60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser
65   70   75   80

Leu Ser Gly Leu

<210> 24

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65)..(316)

<400> 24

agcgtcgcct cacgcggagc agagctgagc tgaagcggga cccggagccc gagcagccgc 60

cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc   109
     Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile
     1   5   10   15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa   157
Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys
                20   25   30

gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag   205
Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln
            35   40   45

att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat   253
Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr
            50   55   60

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac   301
Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His
            65   70   75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa   356
Ser Leu Ser Gly Leu
80

gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggctttagac   416

attggtggga ccaaggatgt tttgcaggat gccctgatcc taagaagggg gcctggggggt 476

gcgtgcagcc tgtcgggggag accccactct gtgcacctat tggctcttct agctgactct 536

tctcgttggg cttagagtct gcctgtttct gctagctccg tgtttagtcc acttgggtca 596

tcagctctgc caagctgagc ctggccaagc taggtggaca gacccttgca gtgatgtccg 656

tttgtccaga ttctgccagt catcactgga cacgtctcct cgcagctgcc ctagcaaggg 716

gagacattgt ggtagctatc agacatggac agaaactgac ttagtgctca caagccccta 776

caccttctgg gctgaagatc acccagctgt gttcagaatt ttcttactgt gcttaggact 836

gcacgcaagt gagcagacac caccgacttc ctttctgcgt caccagtgtc gtcagcagag 896

agaggacagc acaggctcaa ggttggtagt gaagtcaggt tcggggtgca tgggctgtgg 956

tggtggtgat cagttgctcc agtgtttgaa ataagaagac tcatgtttat gtctggaata 1016

agttctgttt gtgctgacag gtgaccttgc tggcagtgct agccaggaaa cagagtgacc 1076

aagggacaag aagggacttg cctaaagcca cccagcaact cagcagcaga accaagatgg 1136

gccccaggct cctccatatg gcccagggct taccaccctta tcacacgtgg ccttgtctag 1196

acccagtcct gagcagggga gaggctcttg agacctgatg ccctcctacc cacatggttc 1256

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tcccactgcc ctgtctgctc tgctgctaca gaggggcagg gcctccccca gcccacgctt 1316

aggaatgctt ggcctctggc aggcaggcag ctgtacccaa gctggtgggc aggggctgg 1376

aaggcaccag gcctcaggag gagccccata gtcccgcctg cagcctgtaa ccatcggctg 1436

ggccctgcaa ggcccacact cacgccctgt gggtgatggt cacggtgggt gggtgggggc 1496

tgaccccagc ttccagggga ctgtcactgt ggacgccaaa atggcataac tgagataagg 1556

tgaataagtg acaaataaag ccagtttttt acaaggt                           1593
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<210> 25

<211> 179

<212> PRT

<213> Homo sapiens

<400> 25

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Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
1               5                   10                  15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
                20                  25                  30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
            35                  40                  45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala
```

```
        50                    55                      60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys
 65                    70                  75                  80


Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln
                     85                  90                  95


Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met
                    100                 105                 110


Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly
                    115                 120                 125


Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile
                    130                 135                 140


Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr
145                 150                 155                 160


Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala
                    165                 170                 175


Leu Leu Phe
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<210> 26

<211> 1820

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114)..(650)

<400> 26

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acgcggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg   116
                                                             Met
                                                              1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg   164
Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro
             5   10   15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg   212
Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu
        20   25   30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc   260
Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro
    35   40   45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt   308
Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val
50   55   60   65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg   356
Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr
                70   75   80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg   404
Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu
            85   90   95

aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc   452
Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val
            100   105   110

cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg   500
His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu
        115   120   125

tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg   548
Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly
130   135   140   145

tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt   596
Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe
                150   155   160

gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg   644
Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu
            165   170   175

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ctc ttc tgagcccgtc tcccggacag gttgaggaag ctgctccaga agcgcctcgg   700

Leu Phe

aaggggagct ctcatcatgg cgcgtgctgc tgcggcatat ggacttttaa taatgttttt 760

gaatttcgta ttctttcatt ccactgtgta aagtgctaga cattttccaa tttaaaattt 820

tgcttttat cctggcactg gcaaaaagaa ctgtgaaagt gaatttattc agccgactgc 880

cagagaagtg ggaatggtat aggattgtcc ccaagtgtcc atgtaacttt tgttttaacc 940

tttgcacctt ctcagtgctg tatgcggctg cagccgtctc acctgtttcc ccacaaaggg 1000

aatttctcac tctggttgga agcacaaaca ctgaaatgtc tacgtttcat tttggcagta 1060

gggtgtgaag ctgggagcag atcatgtatt tcccggagac atgggacctt gctggcatgt 1120

ctccttcaca atcaggcgtg ggaatatctg gcttaggact gtttctctct aagacaccat 1180

tgttttccct tattttaaaa gtgatttttt taaggacaga acttcttcca aaagagaggg 1240

atggctttcc cagaagacac tctggagacc ttgctggcag tgctagccag gaaacagagt 1300

gaccaaggga caagaaggga cttgcctaaa gccacccagc aactcagcag cagaaccaag 1360

atgggcccca ggctcctcca tatggcccag ggcttaccac cctatcacac gtggccttgt 1420

ctagacccag tcctgagcag gggagaggct cttgagacct gatgccctcc tacccacatg 1480

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gttctcccac tgccctgtct gctctgctgc tacaragggg cagggcctcc cccagcccac 1540

gcttaggaat gcttggcctc tggcaggcag gcagctgtac ccaagctggt gggcaggggg 1600

ctggaaggca ccaggcctca ggaggagccc catagtcccg cctgcagcct gtaaccatcg 1660

gctgggccct gcaaggccca cactcacgcc ctgtgggtga tggtcacggt gggtgggtgg 1720

gggctgaccc cagcttccag gggactgtca ctgtggacgc caaaatggca taactsasat 1780

aaggtgaata agtgacaaat aaagccagtt ttttacaagg 1820

<210> 27

<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1   5   10   15

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

             20   25   30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

             35   40   45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

                50   55   60

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65   70   75   80

Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
                85   90   95

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
                100   105   110

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
                115   120   125

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
                130   135   140

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
145   150   155   160

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
                165   170   175

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
                180   185   190

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
                195   200   205

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Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
        210                 215                 220


Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225                 230                 235                 240


Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
                245                 250                 255


Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
            260                 265                 270


Ile Ala Lys Val Lys Ala Asn
            275
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<210> 28

<211> 1472

<212> DNA

<213> Homo sapiens


<220>

<221> CDS

<222> (119)..(955)


<400> 28

gcccagcaga tgaggaagtg gcaggcaggc aggctggccc cggggacttc tctctggccc   60


tgctccctcc gagcgctccg ccgttgcccg cctggcccct acggagtcct tagccagg    118
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```
atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat      166
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
 1               5                   10                  15


ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc      214
Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
                20                  25                  30


tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc      262
Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
            35                  40                  45


atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc      310
Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
        50                  55                  60


tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc      358
Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65                  70                  75                  80


ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg      406
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
                85                  90                  95


gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg      454
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
                100                 105                 110
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ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt      502
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
         115              120              125


att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat      550
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
         130              135              140


cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg      598
His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
145              150              155              160


gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc      646
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
                  165              170              175


ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa      694
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
         180              185              190


ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag      742
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
         195              200              205


ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc      790
Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
         210              215              220


tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc      838
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Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly

225   230   235   240

acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc   886
Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
                  245   250   255

aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt   934
Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
                  260   265   270

att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgcccacc   985
Ile Ala Lys Val Lys Ala Asn
                  275

taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct 1045

gtgaccaagg cttatgtggt caggactgag caggggactg gccctcccct ccccacagct 1105

gctctacagg gaccacggct ttggttcctc acccacttcc cccgggcagc tccagggatg 1165

tggcctcatt gctgtctgcc actccagagc tgggggctaa aagggctgta cagttatttc 1225

cccctccctg ccttaaaact tgggagagga gcactcaggg ctggccccac aaagggtctc 1285

gtggcctttt tcctcacaca gaagaggtca gcaataatgt cactgtggac ccagtctcac 1345

tcctccaccc cacacactga agcagtagct tctgggccaa aggtcagggt gggcgggggc 1405

ctgggaatac agcctgtgga ggctgcttac tcaacttgtg tcttaattaa aagtgacaga 1465

ggaaacc   1472

<210> 29

<211> 137

<212> PRT

<213> Homo sapiens

<400> 29

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1   5   10   15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

            20   25   30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

            35   40   45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

        50   55   60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65   70   75   80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

            85   90   95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
      100   105   110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala
      115   120   125

Tyr Met Asp Ala Pro Lys Ala Ala Leu
      130   135

<210> 30

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145)..(555)

<400> 30

gtgcttcctg tggctgacgt catctggagg agatttgctt tctttttctc caaaaggggga 60

ggaaattgaa actgagtggc ccacgatggg aagagggggaa agcccagggg tacaggaggc 120

ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt   171
                                    Met Gly Phe Gly Ala Thr Leu Ala Val
                                   1   5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc   219

Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe

10   15   20   25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg   267

Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro

              30   35   40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct   315

Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro

              45   50   55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc   363

Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly

              60   65   70

tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca   411

Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro

              75   80   85

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc   459

Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala

90   95   100   105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc   507

Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser

              110   115   120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc   555

Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu

125   130   135

tgagcattcc ctggcctctc tggctgccac ttggttatgt tgtgtgtgtg cgtgagtggt 615

gtgcaggcgc ggttccttac gccccatgtg tgctgtgtgt gtccaggcac ggttccttac 675

gccccatgtg tgctgtgtgt gtcctgcctg tatatgtggc ttcctctgat gctgacaagg 735

tggggaacaa tccttgccag agtgggctgg gaccagactt tgttctcttc ctcacctgaa 795

attatgcttc ctaaaatctc aagccaaact caaagaatgg ggtggtgggg ggcaccctgt 855

gaggtggccc ctgagaggtg ggggcctctc cagggcacat ctggagttct tctccagctt 915

accctagggt gaccaagtag ggcctgtcac accagggtgg cgcagctttc tgtgtgatgc 975

agatgtgtcc tggtttcggc agcgtagcca gctgctgctt gaggccatgg ctcgtccccg 1035

gagttggggg tacccgttgc agagccaggg acatgatgca ggcgaagctt gggatctggc 1095

caagttggac tttgatcctt tgggcagatg tcccattgct ccctggagcc tgtcatgcct 1155

gttggggatc aggcagcctc ctgatgccag aacacctcag gcagagccct actcagctgt 1215

acctgtctgc ctggactgtc ccctgtcccc gcatctcccc tgggaccagc tggagggcca 1275

catgcacaca cagcctagct gcccccaggg agctctgctg cccttgctgg ccctgccctt 1335

cccacaggtg agcagggctc ctgtccacca gcacactcag ttctcttccc tgcagtgttt 1395

tcattttatt ttagccaaac attttgcctg ttttctgttt caaacatkat agttgatatg 1455

agactgaaac ccctggggttg tggagggaaa ttggctcaga gatggacaac ctggcaactg 1515

tgagtccctg cttcccgaca ccagcctcat ggaatatgca acaactcctg taccccagtc 1575

cacggtgttc tggcagcagg gacacctggg ccaatgggcc atctggacca aaggtggggt 1635

gtggggccct ggatggcagc tctggcccag acatgaatac ctcgtgttcc tcctccctct 1695

attactgttt caccagagct gtcttagctc aaatctgttg tgtttctgag tctagggtct 1755

gtacacttgt ttataataaa tgcaatcgtt tgg   1788

<210> 31

<211> 118

<212> PRT

<213> Homo sapiens

<400> 31

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
1   5   10   15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
                20   25   30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

```
              35                    40                    45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
      50                    55                    60


Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
 65                    70                    75                    80


Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
              85                    90                    95


Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
             100                   105                   110


Glu Cys Pro Cys Gln Leu
        115
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<210> 32

<211> 1908

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(444)

<400> 32

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ggaggcctct gggtgaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc   114
                                        Met Gly Phe Gly Ala Thr Leu Ala
                                       1   5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc   162
Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys
      10   15   20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt   210
Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg
25   30   35   40

ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat   258
Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr
              45   50   55

cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag   306
Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln
              60   65   70

ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac   354
Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr
              75   80   85

cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg   402
Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro
      90   95   100

```
gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc          444
Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu
105                 110                 115
```

```
tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac 504
```

```
atcactcaac aggcctctgc ccctttctgc ttgcctgcca ctcacacggc agcccaccat 564
```

```
gctcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624
```

```
agccagcctc cttacaaccc ggcctacatg gatgccccga aggcggccct ctgagcattc 684
```

```
cctggcctct ctggctgcca cttggttatg ttgtgtgtgt gcgtgagtgg tgtgcaggcg 744
```

```
cggttcctta cgccccatgt gtgctgtgtg tgtccaggca cggttcctta cgccccatgt 804
```

```
gtgctgtgtg tgtcctgcct gtatatgtgg cttcctctga tgctgacaag gtggggaaca 864
```

```
atccttgcca gagtgggctg ggaccagact ttgttctctt cctcacctga aattatgctt 924
```

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cctaaaatct caagccaaac tcaaagaatg gggtggtggg gggcaccctg tgaggtggcc 984
```

```
cctgagaggt gggggcctct ccagggcaca tctggagttc ttctccagct taccctaggg 1044
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```
tgaccaagta gggcctgtca caccagggtg gcgcagcttt ctgtgtgatg cagatgtgtc 1104
```

```
ctggtttcgg cagcgtagcc agctgctgct tgaggccatg gctcgtcccc ggagttgggg 1164
```

```
gtacccgttg cagagccagg gacatgatgc aggcgaagct tgggatctgg ccaagttgga 1224
```

```
ctttgatcct ttgggcagat gtcccattgc tccctggagc ctgtcatgcc tgttgggggat 1284


caggcagcct cctgatgcca gaacacctca ggcagagccc tactcagctg tacctgtctg 1344


cctggactgt cccctgtccc cgcatctccc ctgggaccag ctggagggcc acatgcacac 1404


acagcctagc tgcccccagg gagctctgct gcccttgctg gccctgccct tcccacaggt 1464


gagcagggct cctgtccacc agcacactca gttctcttcc ctgcagtgtt ttcattttat 1524


tttagccaaa cattttgcct gttttctgtt tcaaacatga tagttgatat gagactgaaa 1584


cccctgggtt gtggagggaa attggctcag agatggacaa cctggcaact gtgagtccct 1644


gcttcccgac accagcctca tggaatatgc aacaactcct gtaccccagt ccacggtgtt 1704


ctggcagcag ggacacctgg gccaatgggc catctggacc aaaggtgggg tgtggggccc 1764


tggatggcag ctctggccca gacatgaata cctcgtgttc ctcctccctc tattactgtt 1824


tcaccagagc tgtcttagct caaatctgtt gtgtttctga gtctagggtc tgtacacttg 1884


tttataataa atgcaatcgt ttgg                                     1908
```

<210> 33

<211> 168

<212> PRT

86/735

<213> Homo sapiens

<400> 33

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln
1   5   10   15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala
            20   25   30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro
        35   40   45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala
        50   55   60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val
65   70   75   80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro
                85   90   95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala
            100   105   110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro
            115   120   125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly
        130   135   140

```
Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly
145                 150                 155                 160


Ser Asp Gly Gly Tyr Thr Ile Trp
                165
```

<210> 34

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(573)

<400> 34

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ctccgaacag gaagaggacg aaaaaaataa ccgtccgcga cgccgagaca aaccggaccc  60


gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111
          Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro
           1               5                  10


gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct   159
Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro
15                  20                  25                  30


cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat   207
```

```
Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr
                 35                  40                  45


cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca   255
Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser
                 50                  55                  60


gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg   303
Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val
                 65                  70                  75


gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc   351
Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val
             80                  85                  90


ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat   399
Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr
 95                 100                 105                 110


gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct   447
Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
                115                 120                 125


cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg   495
Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
                130                 135                 140


cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg   543
Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met
```

89/735

<pre>
                145   150   155

        ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc   593
        Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp
             160   165

        tgtgccggga aagacatcac ataccttcag cacttctcac aatgtaactg ctttagtcat   653

        attaacctga agttgcagtt tagacacatg ttgttggggt gtctttctgg tgcccaaact   713

        ttcaggcact tttcaaattt aataaggaac catgtaatgg tagcagtacc tccctaaagc   773

        attttgaggt aggggaggta tccattcata aaatgaatgt gggtgaagcc gccctaagga   833

        ttttccttta atttctctgg agtaatactg taccatactg gtctttgctt ttagtaataa   893

        aacatcaaat taggtttgga gggaactttg atcttcctaa gaattaaagt tgccaaatta   953

        ttctgattgg tctttaatct cctttaagtc tttgatatat attacttgtt ataaatggaa   1013

        cgcattagtt gtctgccttt ccttttccat cccttgcccc acccatccca tctccaaccc   1073

        tagtcttcca tttcctcccg ccagtctcca ttgaatcaat ggtgcaggac agaaagccag   1133

        tcagactaat ttccttcttt cctcgcactt ctccccactc gtcatctttt aactagtgtt   1193

        tcacaaggat cctctgaaac cctctctgtg ccccaagtac agatgccatt acttctgctt   1253

        tcgtatctcc tcaggcaaaa gtggagggtg ccttatgggc cctcctcata ggttgtctct   1313
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gcatacacga acctaaccca aatttgcttt ggtgccagaa aaactgagct atgtttgaac 1373

aaagatgtcg tgcaaactgt actgtgaaca acagttggtt taaaatatga ggggcaagga 1433

ggaggatgca tttcaaaagc ttgattgatg tgttcagagc taaattaaga ggagttttca 1493

gatcaaaaac tggttaccat tttttgtcag agtgtctgat gcggccactc attcggctcc 1553

ccagaattcc tagactgggt taatagggtc atattgtgaa tgtctcacta caaaatgact 1613

tgagtccagt gaaatctcat tagggtttaa gaatatttca gggatcctta atgttttgat 1673

ttttgttttc tgaaattgga ttttatttta ttttatctta taatttcagt tcatctaaat 1733

tgtgtgttct gtacatgtga tgtttgactg taccattgac tgttatggaa gttcagcgtt 1793

gtatgtctct ctctacactg tggtgcactt aacttgtgga atttttatac taaaaatgta 1853

gaataaagac tattttgaag atttgaataa agtgatgaag ttgc 1897

<210> 35

<211> 455

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu

```
        1              5                    10                   15


Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
            20                   25                   30


Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
        35                   40                   45


Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
        50                   55                   60


Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
    65                   70                   75                   80


Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
                85                   90                   95


Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe
            100                  105                  110


Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly
        115                  120                  125


Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu
        130                  135                  140


Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
145                  150                  155                  160
```

Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
              165   170   175

Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg
              180   185   190

Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala
              195   200   205

Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
     210   215   220

Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
225   230   235   240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu
              245   250   255

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
              260   265   270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
              275   280   285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
     290   295   300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr
305   310   315   320

Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val
                325   330   335

Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile
                340   345   350

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr
                355   360   365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala
                370   375   380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met
385   390   395   400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu
                405   410   415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val
                420   425   430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala
                435   440   445

Pro Glu Lys Gln Met Ala Pro
450   455

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1480)

<400> 36

agtcccggct gcagcacctg ggagaaggca gaccgtgtga gggggcctgt ggccccagcg 60

tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118
                                                                Met
                                                                 1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166
Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe
            5   10   15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214
Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr
        20   25   30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262
Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala
        35   40   45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310

Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val

50   55   60   65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta   358

Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val

         70   75   80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt   406

Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe

         85   90   95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc   454

Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser

        100   105   110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat   502

Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp

        115   120   125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag   550

Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln

130   135   140   145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt   598

Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu

        150   155   160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc   646

Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe

```
                165                   170                       175


ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg    694
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu
        180               185             190


ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg    742
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met
    195               200             205


gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca    790
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser
210               215             220               225


ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt    838
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser
            230               235             240


gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta    886
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu
            245               250             255


agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag    934
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu
        260               265             270


aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt    982
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu
    275               280             285
```

ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc   1030
Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr
290   295   300   305

atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga   1078
Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg
          310   315   320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag   1126
Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys
          325   330   335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc   1174
Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val
          340   345   350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc   1222
Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala
          355   360   365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag   1270
Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln
370   375   380   385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt   1318
Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser
          390   395   400

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```
atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg    1366
Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu
        405                 410                 415


cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc    1414
Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser
        420                 425                 430


gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca    1462
Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro
    435                 440                 445


gag aag caa atg gca cct tgaacttaag cctactacag actgttagag           1510
Glu Lys Gln Met Ala Pro
450                 455


gccagtggtt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570


ttataaacaa acaaaatgct atggtagcat ttttcacctt catagcatac tccttccccg 1630


tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690


agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggcggagagg 1750


agccaagaaa ctaaaggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810


gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaaaaggt tatagctttg 1870


ccttgagatt gactcattaa aatcagagac tgt                              1903
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<210> 37

<211> 322

<212> PRT

<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser
1   5   10   15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala
                20   25   30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser
                35   40   45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile
        50   55   60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser
65   70   75   80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met
                85   90   95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala
                100   105   110

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp
        115   120   125

Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu
        130   135   140

Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu
145   150   155   160

Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val
                165   170   175

Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp
        180   185   190

Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe
        195   200   205

Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr
        210   215   220

Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu
225   230   235   240

Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly
                245   250   255

Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg
                260   265   270
                        101/735

Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His
        275   280   285

Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser
    290   295   300

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp
305   310   315   320

Phe Gln

<210> 38

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292)..(1257)

<400> 38

tactgctggc ggctggagcg gagcgcaccg cggcggtggt gcccagagcg gagcgcagct 60

ccctgccccg cccctccccc tcggcctcgc ggcgacggcg gcggtggcgg cttggacgac 120

tcggagagcc gagtgaagac atttccacct ggacacctga ccatgtgcct gccctgagca 180

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gcgaggccca ccaggcatct ctgttgtggg cagcagggcc aggtcctggt ctgtggaccc 240


tcggcagttg gcaggctccc tctgcagtgg ggtctgggcc tcggccccac c atg tcg   297
                                                          Met Ser
                                                           1


agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc   345
Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser
            5                   10                  15


acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca   393
Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala
        20                  25                  30


gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca   441
Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala
    35                  40                  45                  50


gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt   489
Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser
                55                  60                  65


gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac   537
Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr
                70                  75                  80


tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc   585
Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly
```

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                  85                    90                    95


gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg    633
Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala Ser Leu
          100                   105                   110


ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc    681
Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser
    115                   120                   125                   130


aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc    729
Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser
                  135                   140                   145


aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg    777
Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu
                  150                   155                   160


cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag    825
Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu
          165                   170                   175


cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag    873
His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu
          180                   185                   190


gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac    921
Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr
195                   200                   205             210
```

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca   969
Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala
                215   220   225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag   1017
Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu
                230   235   240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag   1065
Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys
            245   250   255

aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac   1113
Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn
        260   265   270

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att   1161
Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile
275   280   285   290

tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct   1209
Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala
                295   300   305

ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag   1257
Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
                310   315   320

tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377

tcacagattt cattcctgtt tttatatata tattttttgt tgtcgtttta acatctccac 1437

gtccctagca t 1448

<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn

1 5 10 15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His

20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu

35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys

50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu

65 70 75 80

Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu
                85   90   95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe
                100   105   110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly
                115   120   125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile
                130   135   140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val
145   150   155   160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala
                165   170   175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly
                180   185   190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val
                195   200   205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr
210   215   220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met
                                    107/735

```
          225                  230                  235                  240
```

```
Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser
                     245                  250                  255
```

```
Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu
                     260                  265                  270
```

```
His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro
                     275                  280                  285
```

```
Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys
                     290                  295                  300
```

```
Gln Met His Ile Trp Met Ser Ser Thr
305                  310
```

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(1091)

<400> 40

ggcggaaccg agctgacggg cgtgcggccg ctgcgccgca aactcgtgtg ggacgcaccg 60

ctccagccgc ccgcgggcca gcgcaccggt cccccagcgg cagccgagcc cgcccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac   173
                                 Met Ala Gly Gln Pro Gly His
                                 1   5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct   221
Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro
          10   15   20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc   269
Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg
      25   30   35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag   317
Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln
 40   45   50   55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg   365
Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val
             60   65   70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg   413
Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg
          75   80   85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca   461
Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro

                90   95   100

```
aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac    509
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn
    105                 110                 115
```

```
att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag    557
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys
120                 125                 130                 135
```

```
tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag    605
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys
                140                 145                 150
```

```
tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg    653
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg
                155                 160                 165
```

```
gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg    701
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr
                170                 175                 180
```

```
ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct    749
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser
    185                 190                 195
```

```
gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca    797
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser
200                 205                 210                 215
```

```
ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg    845
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp
            220                 225                 230


tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc    893
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe
            235                 240                 245


tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag    941
Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln
            250                 255                 260


tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga    989
Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg
            265                 270                 275


gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac   1037
Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp
280                 285                 290                 295


atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc   1085
Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser
            300                 305                 310


agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgccttac   1141
Ser Thr


ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201
```

tcagcaggtt ccccaaaagg ctgcccagcc ttacagcaga tgctgaaggc agagcagctg 1261

agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321

gttgtggaca atctcagctg ggtcaataag ggcaggtggt tcagcgagcc acggcagccc 1381

cctgtatctg gattgtaatg tgaatcttta gggtaattcc tccagtgacc tgtcaaggct 1441

tatgctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgagcct ttgaaaatgg 1501

ttagtaccgg gttcagttta gttcttggta tcttttcaat caagctgtgt gcttaattta 1561

ctctgttgta aagggataaa gtggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro
1   5   10   15

Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr
                20   25   30

Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln

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```
                35                    40                         45


     Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
         50                   55                  60


     Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
      65                  70                  75                  80


     Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
                     85                  90                  95


     Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
                    100                 105                 110


     Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
                 115                 120                 125


     Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
         130                 135                 140


     Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
     145                 150                 155                 160


     Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
                     165                 170                 175


     Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
                     180                 185                 190
```

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
      195   200   205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
      210   215   220

Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr
225   230   235   240

Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
         245   250   255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
         260   265   270

Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
         275   280   285

Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
      290   295   300

Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305   310   315   320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
         325   330   335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
         340   345   350

```
Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
        355                 360                 365

Ala Lys Glu
        370
```

<210> 42

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(1203)

<400> 42

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attggccatc accgcgcggc cgcgcagcgg acaccgtgcg taccggcctg cggcgcccgg   60


ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg   114
                                Met Ser His Glu Lys Ser Phe Leu
                                 1               5


gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg   162
Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly
        10                  15                  20


ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc   210
```

Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala

25   30   35   40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg   258

Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly

        45   50   55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt   306

Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly

        60   65   70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc   354

Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly

        75   80   85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat   402

Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr

        90   95   100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc   450

Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe

105   110   115   120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag   498

Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu

        125   130   135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg   546

Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp

```
                140                    145                    150


gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg    594
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val
        155                    160                    165


ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act    642
Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr
      170                    175                    180


ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac    690
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr
185                    190                    195                    200


tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt    738
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys
                205                    210                    215


tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg    786
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser
                220                    225                    230


gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc    834
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe
        235                    240                    245


tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc    882
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val
        250                    255                    260
```

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc   930
Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
265   270   275   280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc   978
Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe
             285   290   295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac   1026
Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
             300   305   310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc   1074
Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
             315   320   325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat   1122
Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
             330   335   340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg   1170
Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
345   350   355   360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
             365   370

gtgcccgctc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283

tacttcccct ctctcttgtc cccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343

ctcctgtatg tacactgcag atacttccat ttggacccgc tgtggccaca gcatggcccc 1403

tttagtcctc ccgcccccgc caaggggcag caaggccacg tttccgtgcc acctcctgtc 1463

tactcattgt tgcatgagcc ctgtctgcca gcccacccca gggactgggg gcagcaccag 1523

gtcccgggga gagggattga gccaagaggt gagggtgcac gtcttccctc ctgtcccagc 1583

tccccagcct ggcgtagagc acccctcccc tccccccac ccccctggag tgctgccctc 1643

tggggacatg cggagtgggg gtcttatccc tgtgctgagc cctgagggca gagaggatgg 1703

catgtttcag gggaggggga agccttcctc tcaatttgtt gtcagtgaaa ttccaataaa 1763

tgggatttgc tctctgcc   1781

<210> 43

<211> 393

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
1   5   10   15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
           20   25   30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
           35   40   45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
           50   55   60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
 65   70   75   80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
                85   90   95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
          100   105   110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
          115   120   125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
          130   135   140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145   150   155   160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
                              120/735

```
              165                 170                 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
             180                 185                 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
             195                 200                 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
             210                 215                 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225                 230                 235                 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
                 245                 250                 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
                 260                 265                 270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
             275                 280                 285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
290                 295                 300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
305                 310                 315                 320
```

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Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
325 330 335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
340 345 350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
355 360 365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
370 375 380

Leu Val Pro Gly Pro Glu Lys Glu Asn
385 390

<210> 44

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 44

agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac 58

Met Ser Asp

1

●

```
gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg      106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
     5               10              15


cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc      154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
 20              25              30              35


gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta      202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
             40              45              50


gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg      250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
             55              60              65


ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg      298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
             70              75              80


cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg      346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
     85              90              95


tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg      394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100             105             110             115
```

```
ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga      442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
                120                 125                 130


gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg      490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
                135                 140                 145


act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt      538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
                150                 155                 160


gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc      586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
                165                 170                 175


ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac      634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
180                 185                 190                 195


atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca      682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
                200                 205                 210


gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag      730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
                215                 220                 225


gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act      778
```

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Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
     230   235   240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att   826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
     245   250   255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc   874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
260   265   270   275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg   922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
                 280   285   290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat   970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
                 295   300   305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg   1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
                 310   315   320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt   1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
     325   330   335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag   1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
                              125/735

```
        340                 345                 350                 355


ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg   1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
                    360                 365                 370


aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca   1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
                375                 380                 385


ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac          1258
Gly Pro Glu Lys Glu Asn
            390


cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318


ctgtcataat gctctgccct ccctcccccg aagttctctg tggtgatgac cgctctcccc 1378


tgcccctccc cgcttcctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438


ccctgccaag gcgacaggga gggtcagagg gaggccggct gcttcctgcc cccacccttt 1498


ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtcccccctg ttgtgttcca 1558


tgtgctttca cctctgcctc atctttcctc ccgtccctgc cccgccacct ccccaaagaa 1618


ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct 1678


ccctagtgtc ccttcagcct gggctgacca gtgcccgcct ctgggcttga ccagttccca 1738
```

atctcgtcct ctgtccccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798

ctgccattct taaccaaggc agccccaagc ctcctgggga ggcagggcaa aaacaggtgc 1858

cctcatcgtg gtctgtgcca tgtcccgtct ctatggtggt tgaggagaaa ggcgggggaag 1918

cttcctcagc cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgct 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038

gaggccctac tgccttctca aagcagagag gcagcttatc aaactcagcc caaaactctg 2098

tttacatggg tggggagatg gagcagggaa gtacagagtg ggatggtcag gacctgggcc 2158

attgcaacca aaatggggac ttcctgggta gggaggtcac tccctctact cactgagcta 2218

ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278

tcctcattgt ctaaatgagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45

<211> 393

<212> PRT

<213> Homo sapiens

<400> 45

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Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
 1               5                  10                  15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
                20                  25                  30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
            35                  40                  45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
            50                  55                  60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
65                  70                  75                  80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
                85                  90                  95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
                100                 105                 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
            115                 120                 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
    130                 135                 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
```

145   150   155   160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
          165   170   175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
        180   185   190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
        195   200   205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
      210   215   220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225   230   235   240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
        245   250   255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
        260   265   270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
        275   280   285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
        290   295   300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
305   310   315   320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
          325   330   335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
          340   345   350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
          355   360   365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
          370   375   380

Leu Val Pro Gly Pro Glu Lys Gln Asn
385   390

<210> 46

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 46

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agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac   58
                                                           Met Ser Asp
                                                            1
```

```
gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg   106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
     5              10              15
```

```
cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc   154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
 20              25              30              35
```

```
gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta   202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
             40              45              50
```

```
gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg   250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
                 55              60              65
```

```
ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg   298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
                 70              75              80
```

```
cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg   346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
         85              90              95
```

```
tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg   394
```

```
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100             105             110             115
```

```
ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga     442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
                120             125             130
```

```
gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg     490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
            135             140             145
```

```
act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt     538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
            150             155             160
```

```
gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc     586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
            165             170             175
```

```
ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac     634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
180             185             190             195
```

```
atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca     682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
                200             205             210
```

```
gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag     730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
                132/735
```

                215   220   225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act   778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
        230   235   240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att   826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
        245   250   255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc   874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
260   265   270   275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg   922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
                280   285   290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat   970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
                295   300   305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg   1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
        310   315   320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt   1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
        325   330   335

```
ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag   1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
340                 345                 350                 355


ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg   1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
                    360                 365                 370


aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca   1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
                375                 380                 385


ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac         1258
Gly Pro Glu Lys Gln Asn
            390


cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318


ctgtcataat gctctgccct ccctcccccg aagttctctg tggtgatgac cgctctcccc 1378


tgcccctccc cgcttcctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438


ccctgccaag gcgacaggga gggtcagagg gaggccggct gcttcctgcc cccacccttt 1498


ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtcccccctg ttgtgttcca 1558


tgtgctttca cctctgcctc atctttcctc ccgtccctgc cccgccacct ccccaaagaa 1618
```

```
ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct 1678


ccctagtgtc ccttcagcct gggctgacca gtgcccgcct ctgggcttga ccagttccca 1738


atctcgtcct ctgtccccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798


ctgccattct taaccaaggc agccccaagc ctcctgggga ggcagggcaa aaacaggtgc 1858


cctcatcgtg gtctgtgcca tgtcccgtct ctatggtggt tgaggagaaa ggcggggaag 1918


cttcctcagc cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgct 1978


gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038


gaggccctac tgccttctca aagcagagag gcagcttatc aaactcagcc caaaactctg 2098


tttacatggg tggggagatg gagcagggaa gtacagagtg ggatggtcag gacctgggcc 2158


attgcaacca aaatggggac ttcctgggta gggaggtcac tccctctact cactgagcta 2218


ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278


tcctcattgt ctaaatgagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338


accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg   2396
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<210> 47

<211> 138

<212> PRT

<213> Homo sapiens

<400> 47

Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly
1   5   10   15

Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys
                20   25   30

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
                35   40   45

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys
        50   55   60

Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile
65   70   75   80

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
                85   90   95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val
                100   105   110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
                115   120   125

Asp Lys Val Gly Glu Ser Asn Asn Met Val

130   135

<210> 48

<211> 2976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110)..(523)

<400> 48

agacgtggcg gctctcgcct gggctgtttc ccggcttcat ttctcccgac tcagcttccc 60

accctgggct ttccgaggtg ctgtcgccgc tgtccccacc actgcagcc atg atc tcc 118

                                                        Met Ile Ser
                                                         1

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg   166
Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val
        5   10   15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg   214
Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu
    20   25   30   35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt   262
Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly

```
                    40                      45                      50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct    310
Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala
            55                      60                      65


aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct    358
Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro
            70                      75                      80


ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg    406
Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg
            85                      90                      95


ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt    454
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu
100                 105                 110                 115


gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt    502
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val
                    120                 125                 130


gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta    553
Gly Glu Ser Asn Asn Met Val
                    135


aaatattgtg ttatttataa agtcatttga agaatattca gcacaaaatt aaattacatg 613


aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673
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caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733

caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc ttgaaggcta 793

tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc ttagagaact gtggtgcctg 853

tttcttttct ttttattttg aaggctcagg agcatccata ggcatttgct ttttagaaat 913

gtccactgca atggcaaaaa tatttccagt tgcactgtat ctctggaagt gatgcatgaa 973

ttcgattgga ttgtgtcatt ttaaagtatt aaaaccaagg aaaccccaat tttgatgtat 1033

ggattacttt tttttgtaaa catggttaaa ataaaacttc tgtggttctt ctgaatctta 1093

atatttcaaa gccaggtgaa aatctgaact agatattctt tgttggaata tgcaaaggtc 1153

attctttact aactttagt tactaaatta tagctaagtt ttgtcagcag catactccgg 1213

aaagtctcat acttcttggg agtctgccct cctaagtatc tgtctatatc attcattacg 1273

tgtaagtatt taacaaaaaa gcattcttga ccatgaatga agtagtttgt ttcatagctt 1333

gtctcattga atagtattat tgaagatact aaatgatgca aaccaaatgg atttttccca 1393

tgtcatgatg taatttttct ttcttctttc tttttttaa attttagcag tggcttatta 1453

tttgttttc ataaattaaa ataacttttg ataatgttta ctttaagaca tgtaacatgt 1513

139/735

```
taaaaggtta aacttatggc tgtttttaaa gggctattca tttaatctga gttttcccctt 1573

attttcagct ttttcctagc atataatagt cattaagcat gacatatcct tcatatgatc 1633

actcatcttg agttaattag aaaatacctg agttcacgtg ctaaagtcat ttcactgtaa 1693

taaactgact atggtttctt aagaacatga cactaaaaaa aaagtggttt ttttccaccg 1753

ttgctgatta ttagacagta ggaaatagct gttttcttta gttttacaag atgtgacagc 1813

tttagtggta gatgtaggga aacatttcaa cagccatagt actatttgtt ttaccactga 1873

ttgcactgtt ttgtttttttt aacagttgca aagctttta atgcataaaa gtataattga 1933

aatctgtggt atttatttac aaacatgtct acaaaaatag attacagctt attttatttt 1993

tagttaaatc tcttaataca cagagaactc ccaatcttgc tcatctaaat aaggaaagac 2053

ttggtgtata gtgtgatggt ttagtcttaa ggattaagac atttttggta cttgcatttg 2113

acttacgatg tatctgtgaa aatgggatga tattgacaaa tggagactcc tacctcaata 2173

gttaatggaa taataagagg ctactgttgt gtctaatgtt cttcaaaaaa gtaatatcct 2233

cacttggaga gtgtcaaata catactttga ggattgactt tatataaggt gccctgtaga 2293

actctgttac acatattttt gacccatatt atttacaatg tcttgataat tctacctttt 2353

tagagcaaga atagtatctg ctaatgtaag ggacatctgt atttaactcc tttgtagaca 2413
```

tgaatttcta tcaaaatgtt ctttgcactg taacagagat tccttttttc aataatctta 2473

attcaaaagc attattagac ttgaaagggt ttgataatct cccagtcctt agtaaagatt 2533

gagagaggct ggagcagttt tcagttttaa atgagtctgc agttaatatc aaatgtgagt 2593

ttgggactgc ctggcaacat ttatatttct tattcagaac ccttgatgag actatttta 2653

aacatactag tctgctgata gaaagcacta tacatcctat tgtttctttc tttccaaaat 2713

cagccttctg tctgtaacaa aaatgtactt tatagagatg gaggaaaagg tctaatacta 2773

catagcctta agtgtttctg tcattgttca agtgtatttt ctgtaacaga aacatatttg 2833

gaatgttttt cttttcccct tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893

cccactgtca gattatatta tctaacaatt gaatattgta aatatacttg tcttacctct 2953

caataaaagg gtacttttct att   2976

<210> 49

<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe

```
      1              5                    10                   15

His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln
              20                    25                   30

Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val
              35                    40                   45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro
          50                    55                   60

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met
      65                    70                   75                   80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile
                  85                    90                   95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser
              100                   105                  110

Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu
              115                   120                  125

His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp
          130                   135                  140

Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
145                   150                   155                  160
```

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Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
             165   170   175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
             180   185   190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu
             195   200   205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
             210   215   220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
225   230   235   240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser
             245   250   255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
             260   265   270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
             275   280   285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
             290   295   300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
305   310   315   320

```
Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser
            325                 330                 335


Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser
            340                 345                 350


Arg Ser Thr Thr His Leu Ile
            355
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<210> 50

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (327)..(1403)

<400> 50

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aacgtggtgg acctatcctt gcaccagagg agattaagac tattttggt agcatcccag 180

atatctttga tgtacacact aagataaagg atgatcttga agaccttata gttaattggg 240

atgagagcaa aagcattggt gacatttttc tgaaatattc aaaagatttg gtaaaaacct 300

accctccctt tgtaaacttc tttgaa atg agc aag gaa aca att att aaa tgt 353
                    Met Ser Lys Glu Thr Ile Ile Lys Cys
                      1   5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401
Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala
10   15   20   25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449
Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro
               30   35   40

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497
Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys
               45   50   55

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545
His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile
                 60   65   70

gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa 593
Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys
           75   80   85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641
Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly
90   95   100   105

```
tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt   689
Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val
                110               115               120


gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta   737
Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val
                125               130               135


act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac   785
Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His
                140               145               150


aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca   833
Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro
        155               160               165


gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag   881
Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys
170               175               180               185


gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg   929
Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu
                190               195               200


ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag   977
Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln
            205               210               215
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atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt      1025
Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys
        220             225             230


cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att      1073
Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile
        235             240             245


tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac      1121
Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp
250             255             260             265


agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag      1169
Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys
        270             275             280


gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga      1217
Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg
        285             290             295


agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc      1265
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser
        300             305             310


agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta      1313
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu
        315             320             325


gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa      1361
```

Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu
330   335   340   345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata   1403
Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
            350   355

tgaagcgtta ccaaaatctt aaattataga aatgtataga cacctcatac tcaaataaga 1463

aactgactta aatggtactt gtaattagca cttggtgaaa gctggaagga agataaataa 1523

cactaaacta tgctatttga tttttcttct tgaaagagta aggtttacct gttacatttt 1583

caagttaatt catgtaaaaa atgatagtga ttttgatgta atttatctct tgtttgaatc 1643

tgtcattcaa aggccaataa tttaagttgc tatcagctga tattagtagc tttgcaaccc 1703

tgatagagta aataaatttt atgggcgggt gccaaatact gctgtgaatc tatttgtata 1763

gtatccatga atgaatttat ggaaatagat atttgtgcag ctcaatttat gcagagatta 1823

aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883

ttcacatgtg cagtttgaag tatttaaata accactcctt tcacagttta ttttcttctc 1943

aagcgttttc aagatctagc atgtggattt taaaagattt gccctcatta acaagaataa 2003

catttaaagg agattgtttc aaaatatttt tgcaaattga gataaggaca gaaagattga 2063

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gaaacattgt atattttgca aaaacaagat gtttgtagct gtttcagaga gagtacggta 2123


tatttatggt aattttatcc actagcaaat cttgatttag tttgatagtg tgtggaattt 2183


tattttgaag gataagacca tgggaaaatt gtggtaaaga ctgtttgtac ccttcatgaa 2243


ataattctga agttgccatc agttttacta atcttctgtg aaatgcatag atatgcgcat 2303


gttcaacttt ttattgtggt cttataatta aatgtaaaat tgaaaattca tttgctgttt 2363


caaagtgtga tatctttcac aatagccttt ttatagtcag taattcagaa taatcaagtt 2423


catatggata aatgcatttt tatttcctat ttctttaggg agtgctacaa atgtttgtca 2483


cttaaatttc aagtttctgt tttaatagtt aactgactat agattgtttt ctatgccatg 2543


tatgtgccac ttctgagagt agtaaatgac tctttgctac attttaaaag caattgtatt 2603


agtaagaact ttgtaaataa atacctaaaa ccc                                2636
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<210> 51

<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu
1   5   10   15

Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
              20   25   30

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
              35   40   45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
              50   55   60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65   70   75   80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val
                   85   90   95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys
                   100   105   110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
              115   120   125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
              130   135   140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
145   150   155   160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg
                              150/735

Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln
     180   185   190

Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys
     195   200   205

Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe
     210   215   220

Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe
225   230   235   240

Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr
     245   250   255

Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu
     260   265   270

Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys
     275   280   285

Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu
     290   295   300

Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met
305   310   315   320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
                325   330   335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu
                340   345   350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe
                355   360   365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser
                370   375   380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp
385   390   395   400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro
                405   410   415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
                420   425   430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
                435   440   445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
                450   455   460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
465   470   475   480
                        152/735

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp

485   490   495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu

500   505   510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu

515   520   525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu

530   535   540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu

545   550   555   560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu

565   570   575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr

580   585   590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn

595   600   605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val

610   615   620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser

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625   630   635   640

Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp
                645   650   655

Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile
            660   665   670

Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly
            675   680   685

Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu
        690   695   700

Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His
705   710   715   720

Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val
                725   730   735

Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp
            740   745   750

Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp
            755   760   765

Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn
        770   775   780

Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys
785   790   795   800

Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro
                805   810   815

Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu
                820   825   830

Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser
                835   840   845

Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu
                850   855   860

Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr
865   870   875   880

His Leu Ile

<210> 52

<211> 3910

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (29)..(2677)

<400> 52

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                                Met Ala Glu Asn Ser Val Leu Thr

                               1   5

tcc act act ggg agg act agc ttg gca gac tct tcc att ttt gat tct   100
Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser
    10   15   20

aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca   148
Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser
25   30   35   40

tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt   196
Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val
        45   50   55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att   244
Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile
        60   65   70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg   292
Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu
        75   80   85

gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat   340
Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp

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              90                    95                   100


          tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca    388
          Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro
          105                 110                 115                 120


          cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca    436
          Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser
                          125                 130                 135


          tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt    484
          Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe
                          140                 145                 150


          act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc    532
          Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val
                      155                 160                 165


          cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca    580
          His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr
              170                 175                 180


          cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg    628
          His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val
          185                 190                 195                 200


          agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg    676
          Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp
                          205                 210                 215
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gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga     724
Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg
                220                 225                 230


aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg     772
Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu
                235                 240                 245


gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg     820
Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met
        250                 255                 260


caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt     868
Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu
265                 270                 275                 280


gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag     916
Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys
                285                 290                 295


aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg     964
Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met
                300                 305                 310


gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act     1012
Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr
                315                 320                 325
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cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac   1060
Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn
    330   335   340

agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca   1108
Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser
345   350   355   360

aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct   1156
Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala
                365   370   375

gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca   1204
Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro
                380   385   390

gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct   1252
Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser
    395   400   405

tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa   1300
Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln
    410   415   420

gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg   1348
Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu
425   430   435   440

gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa   1396

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            Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln
                            445                 450                 455


cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt    1444
Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly
                460                 465                 470


agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt    1492
Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu
            475                 480                 485


gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att    1540
Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile
        490                 495                 500


ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta    1588
Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val
505                 510                 515                 520


aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag    1636
Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln
                525                 530                 535


aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa    1684
Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu
                540                 545                 550


tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg    1732
Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg
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tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct   1780
Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala
    570             575             580


gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg   1828
Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu
585             590             595             600


aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct   1876
Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala
                605             610             615


caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct   1924
Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala
            620             625             630


aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att   1972
Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile
            635             640             645


tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc   2020
Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe
    650             655             660


ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att   2068
Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile
665             670             675             680
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ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt    2116
Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu
            685                 690                 695


aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac    2164
Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp
            700                 705                 710


ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg    2212
Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg
            715                 720                 725


cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca    2260
Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser
        730                 735                 740


gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta    2308
Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val
745                 750                 755                 760


gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct    2356
Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala
            765                 770                 775


gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg    2404
Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu
            780                 785                 790
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agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga      2452
Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg
            795                 800                 805


gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt      2500
Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu
        810                 815                 820


atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat      2548
Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp
825                 830                 835                 840


aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc      2596
Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile
                845                 850                 855


cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt      2644
Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser
            860                 865                 870


cat acg tta agt aga tct aca act cat ttg ata tgaagcgtta ccaaaatctt   2697
His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
        875                 880


aaattataga aatgtataga cacctcatac tcaataaga aactgactta aatggtactt    2757


gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga   2817


tttttcttct tgaaagagta aggtttacct gttacatttt caagttaatt catgtaaaaa   2877
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atgatagtga ttttgatgta atttatctct tgtttgaatc tgtcattcaa aggccaataa 2937

tttaagttgc tatcagctga tattagtagc tttgcaaccc tgatagagta aataaatttt 2997

atgggcgggt gccaaatact gctgtgaatc tatttgtata gtatccatga atgaatttat 3057

ggaaatagat atttgtgcag ctcaatttat gcagagatta aatgacatca taatactgga 3117

tgaaaacttg catagaattc tgattaaata gtgggtctgt ttcacatgtg cagtttgaag 3177

tatttaaata accactcctt tcacagttta ttttcttctc aagcgttttc aagatctagc 3237

atgtggattt taaaagattt gccctcatta acaagaataa catttaaagg agattgtttc 3297

aaaatatttt tgcaaattga gataaggaca gaaagattga gaaacattgt atattttgca 3357

aaaacaagat gtttgtagct gtttcagaga gagtacggta tatttatggt aattttatcc 3417

actagcaaat cttgatttag tttgatagtg tgtggaattt tattttgaag gataagacca 3477

tgggaaaatt gtggtaaaga ctgtttgtac ccttcatgaa ataattctga agttgccatc 3537

agttttacta atcttctgtg aaatgcatag atatgcgcat gttcaacttt ttattgtggt 3597

cttataatta aatgtaaaat tgaaaattca tttgctgttt caaagtgtga tatctttcac 3657

aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717
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tatttcctat ttctttaggg agtgctacaa atgtttgtca cttaaatttc aagtttctgt 3777

tttaatagtt aactgactat agattgtttt ctatgccatg tatgtgccac ttctgagagt 3837

agtaaatgac tctttgctac attttaaaag caattgtatt agtaagaact ttgtaaataa 3897

atacctaaaa ccc 3910

<210> 53

<211> 622

<212> PRT

<213> Homo sapiens

<400> 53

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Met Gly Pro Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly
1               5                   10                  15

Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn
                20                  25                  30

Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser
        35                  40                  45

Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg
    50                  55                  60

Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys
65                  70                  75                  80
```

```
Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp
                85                  90                  95

Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly
                100                 105                 110

Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His
                115                 120                 125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu
            130                 135                 140

Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln
145                 150                 155                 160

His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn
                165                 170                 175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys
                180                 185                 190

Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser
                195                 200                 205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala
            210                 215                 220

Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly
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225   230   235   240

Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met
                245   250   255

Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu
                260   265   270

Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln
                275   280   285

Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp
                290   295   300

Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys
305   310   315   320

Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg
                325   330   335

Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu
                340   345   350

Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe
                355   360   365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile
                370   375   380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly
385   390   395   400

Phe Thr Lys Ala Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu
                405   410   415

Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu
                420   425   430

Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys
            435   440   445

Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly
        450   455   460

Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met
465   470   475   480

Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
                485   490   495

Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln
                500   505   510

Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
            515   520   525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln
        530   535   540

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Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys
545   550   555   560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr
               565   570   575

Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys
               580   585   590

Phe Gly Leu Val Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr
               595   600   605

Met Val Phe His Pro Ala Arg Glu Lys Val Leu Arg Ser Val
610   615   620

<210> 54

<211> 2426

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (104)..(1969)

<400> 54

gcgccagcag gaagtgggag aagaggcgac ccaaggcggg ctggcgggct ggcggcagtc 60

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gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg     115
                                              Met Glu Gly Pro
                                                        1


ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca     163
Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro
 5                  10                  15                  20


gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc     211
Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala
                    25                  30                  35


aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac     259
Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp
                40                  45                  50


att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg     307
Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu
                55                  60                  65


gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg     355
Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser
             70                  75                  80


ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt     403
Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe
 85                  90                  95                 100


tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat     451
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Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn
            105   110   115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc   499
Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val
            120   125   130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag   547
Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu
            135   140   145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att   595
Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile
            150   155   160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta   643
Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val
165   170   175   180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca   691
Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro
            185   190   195

gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt   739
Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val
            200   205   210

gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga   787
Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly
                        171/735

```
                215                   220                   225


aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat   835
Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp
    230                   235                   240


atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac   883
Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn
245                   250                   255                   260


aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga   931
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg
                265                   270                   275


gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc   979
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu
                280                   285                   290


ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac  1027
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr
        295                   300                   305


ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta  1075
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu
    310                   315                   320


gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg  1123
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly
325                   330                   335                   340
```

tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt   1171
Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val
               345   350   355

ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca   1219
Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala
               360   365   370

gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta   1267
Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu
               375   380   385

tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct   1315
Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala
               390   395   400

tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc   1363
Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly
405   410   415   420

tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca   1411
Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro
               425   430   435

tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat   1459
Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr
               440   445   450

```
gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat     1507
Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His
        455                 460                 465


cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg     1555
His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp
        470                 475                 480


att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca     1603
Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr
485                 490                 495                 500


ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt     1651
Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys
                505                 510                 515


tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca     1699
Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser
            520                 525                 530


tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg     1747
Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu
        535                 540                 545


ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat     1795
Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His
        550                 555                 560


atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc     1843
```

```
                Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe
                565                 570                 575                 580


atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg      1891
Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val
                    585                 590                 595


aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac      1939
Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His
                    600                 605                 610


cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaag caacccaaaa         1989
Pro Ala Arg Glu Lys Val Leu Arg Ser Val
                    615                 620


ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaag tgaagtaaag 2049


atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa 2109


aagttctcaa taaaggcatt acaatttttt aggtttagaa agatggactt ttctgataaa 2169


tcttggcaga catctaaaaa aaaaaccata tttttcacaa gaaaatgcaa gttacttttt 2229


ttggaaataa tactcactga ttatggataa aatggaatat tttcagatac tatattggct 2289


gtttcaaaat agtactattc tttaaacttg taatttttgc taagttattt gtctttgttg 2349


tatctataaa tatgtaaaaa atatttaaat agatgtacct gttttgcttt cacacttaat 2409
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<210> 55

<211> 257

<212> PRT

<213> Homo sapiens

<400> 55

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
1   5   10   15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
            20   25   30

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
            35   40   45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
        50   55   60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
65   70   75   80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
                85   90   95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
            100   105   110

Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly
      115   120   125

Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly
      130   135   140

Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln
145   150   155   160

His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly
              165   170   175

Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu
              180   185   190

Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala
              195   200   205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr
      210   215   220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu
225   230   235   240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp
              245   250   255

Gly

<210> 56

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10)..(780)

<400> 56

tttcccaag atg gcg tcg aag ata ggt tcg aga cgg tgg atg ttg cag ctg 51

        Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu

        1   5   10

atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99

Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly

15   20   25   30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147

Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg

           35   40   45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195

Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala

           50   55   60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc   243
Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe
          65   70   75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac   291
Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr
        80   85   90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac   339
Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr
  95   100   105   110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt   387
Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly
           115   120   125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc   435
Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser
          130   135   140

acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca   483
Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser
        145   150   155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca   531
Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro
     160   165   170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg   579

```
Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu
175             180             185             190


gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc      627
Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile
                195             200             205


ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt      675
Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val
                210             215             220


gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag      723
Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys
            225             230             235


ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc      771
Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala
        240             245             250


act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc              820
Thr Asp Gly
255


actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttattt atgctttttg 880


gtctgtttgt ttgatctttt gctttttttaa aattgttttt tgcagttaag aggcagctca 940


tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000
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caggtttttt tcctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060

gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

aaggaagatg gagattggaa gtgagcaaat gtgaaaaatt cctctttgaa cctggcagat 1180

gcagctaggc tctgcagtgc tgtttggaga ctgtgagagg gagtgtgtgt gttgacacat 1240

gtggatcagg cccaggaagg gcacaggggc tgagcactac agaagtcaca tgggttctca 1300

gggtatgcca ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360

accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420

tgctgtctct gtttctagct ccatggttgg cctggtgggg gtggagttcc ctcccaaaca 1480

ccagaccaca cagtcctcca aaaataaaca ttttatatag   1520

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln

 1   5   10   15

Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys
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            20                    25                    30
```

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu

```
        35                    40                    45
```

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe

```
    50                    55                    60
```

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile

```
65                    70                    75                    80
```

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His

```
            85                    90                    95
```

Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val

```
            100                   105
```


<210> 58

<211> 1496

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)..(329)

<400> 58

ctaccagg atg gct ctc ttc gct ggt ggc aaa ctg cgt gtg cat ctc gac   50

```
                    Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp
                     1                 5                    10


    atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa      98
    Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys
     15                 20                   25                  30


    gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag     146
    Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln
                    35                   40                  45


    gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag     194
    Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu
                    50                   55                  60


    cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg     242
    Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp
                    65                   70                  75


    tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg     290
    Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met
                    80                   85                  90


    cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc     339
    Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
     95                 100                  105


    tttgtatgac ccttcctttt tacctcattt atttggtact ttccccacac agtcctttat 399
```

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ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459

caaaccattc agatcagcca cttgctgacc ctggttctta aggacacatg acattagtcc 519

aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaaccca ggactcagtc 579

ctgcttcttt tgcctcgagt gattttcctc tgtttttcac taaataagca aatgaaaact 639

ctctccatta ccttctgctt tctctttgtc cacttacgca gtaggtgact ggcatgtgcc 699

acagagcagg ccctgcctca ctgtctgctg gtcagttctg ggttcactta atggctttgt 759

gaatgtaaat aaggggcagg tcttggccct agaggattga gatgttttc tatatcttag 819

aactattttt ggataaatta tatattttcc ttcctagtag aagtgttact gcctgtaact 879

agctcaaaat accaatgcag tttctgcatt ctgggttttg tttttctttt tttttttttt 939

tttttttgagt tttgctcttg tcgcccaggc tggagtgcaa tggcgtgatc tcagctcact 999

ggcaacatct gcctcccggg ttcaaatgat tctcctgcct cagtctcctg agtagctggg 1059

attacaggtg cccgccacca cgctcagcta atttttgtat ttttagtaga gatggggttt 1119

taccatgttg gccaggctgg tcttagactc ctgacctcag ttgatccacc tgcctcagcc 1179

tctgcattca gtttattcac atatttttgg taactcccat ggcagctcct aggatttcag 1239

cggtctgtgg gccagaaagc aggcaccagg gctgacctca aggccgtatc agagggccaa 1299

gcagagttct tttggatacc tgcttttcat cccacagggc cttagagtca gaggtaaggt 1359

agcaacagag ctagaatggg gcaatgcact cttaccctcc ttctcaactt ttatttaagc 1419

tgtgctaaat gttttcttca agggaaccag atttagttct ttacagaatt ttccagtgaa 1479

ataaaacatg ttgtaat 1496

<210> 59

<211> 272

<212> PRT

<213> Homo sapiens

<400> 59

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Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly
 1               5                  10                  15


Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp
             20                  25                  30


Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met
             35                  40                  45


Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly
         50                  55                  60


Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln
```

```
         65                  70                  75                  80

Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr
                 85                  90                  95

Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr
                100                 105                 110

Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys
                115                 120                 125

Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg
                130                 135                 140

Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu
145                 150                 155                 160

His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro
                165                 170                 175

Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val
                180                 185                 190

Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr
                195                 200                 205

Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu
                210                 215                 220
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Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln

225   230   235   240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu

         245   250   255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu

         260   265   270

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (117)..(932)

<400> 60

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gccgccgccg ctgcttcagc ttattccttg tggcctctgc gggtcctgcc tcagcc atg 119

                                                    Met

                                                    1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc   167

Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro

         5   10   15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg   215
Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val
       20   25   30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg   263
Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met
       35   40   45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att   311
Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile
50   55   60   65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga   359
Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly
           70   75   80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag   407
Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu
          85   90   95

ggt gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca   455
Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr
      100   105   110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt   503
Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val
      115   120   125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa   551
Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu
130   135   140   145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat   599
Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His
                 150   155   160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct   647
Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser
                 165   170   175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt   695
Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu
                 180   185   190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac   743
Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr
                 195   200   205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg   791
Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met
210   215   220   225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat   839
His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr
                 230   235   240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga   887

Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg
     245   250   255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa   932
Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
     260   265   270

taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatttgta 992

aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct 1052

taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgtactg 1112

tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172

aaattatcac aaagtgggac ctcagcagta gtgatgtgtg tgtctcatga gcagtgagca 1232

cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca 1292

aatcccaatg ccttgtgact ttcataggat tcctgatcat gcatgttgat gtactggctc 1352

ttcactttgg gctttctgat gtttattcac acctttggag agttgcaact tgccacatac 1412

gaaattagtc tcatagtgta gtgaacttca accccaaaat tttaaaaatg tatttccccc 1472

cagttttaaa ttgcctttga aatttaaaaa aaaaaattta gacttagtac cagaaccaaa 1532

aatacctaga tttttggaga acttattaca tacatagaaa catgaatatg gtttaccwct 1592

gtgtgtgtgt gtgtgtgtgt gtgtatacag actttttttt ttaacttgtt gattcagatg 1652

tcttggtccc tgaatagtcc tagattactt attttgagaa ttgattgtta aaaattacag 1712

ggaattaaaa taattgcctt ttttttttta gagggtaaga gatgggtaga agagtatgcc 1772

tctgaaaatt ttattagttt attcttgtgg agaataccaa gaaaatgtgt atttgcccat 1832

tgctaaatat gatatatgcc attttgtatt tatttgtccc aagtgtcttt ttttaagagg 1892

agaataaaca ataaggaatt actg   1916

<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Ser
1   5   10   15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp
            20   25   30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln
        35   40   45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys

                50   55   60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp
        65   70   75   80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile
                    85   90   95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly
                    100   105   110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile
                    115   120   125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu
            130   135   140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu
145   150   155   160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala
                    165   170   175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile
                    180   185   190

Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val
                    195   200   205

Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser

    210   215

<210> 62

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49)..(705)

<400> 62

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                                                  Met Asn Arg

                                                   1

ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac   105

Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp

     5   10   15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att   153

Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile

20   25   30   35

tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag   201

Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys

         40   45   50

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atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga    249
Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg
            55                  60                  65


gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc    297
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala
            70                  75                  80


caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg    345
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu
            85                  90                  95


aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa    393
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu
100                 105                 110                 115


atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta    441
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu
            120                 125                 130


caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa    489
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu
            135                 140                 145


gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta    537
Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu
            150                 155                 160
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gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac    585
Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp
        165             170             175


agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt    633
Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly
180             185             190             195


gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt    681
Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe
                200             205             210


gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta    735
Gly Leu Pro Gln Ile Pro Ala Ser
                215


aaacaaacac atattatggg actaggaaat atttatcttt ccaaatttgc cataacagat    795


ttaggtttct ttcctttctt tgaaggaaag tttaattaca ttgctctttt attttttcca    855


ttaagagact cattgcttgg gaaatgcttt cttcgtacta aaatttgatt cctttttttt    915


cttatgaaaa acgaactcag tttaaaagta tttttagctc gtatgacttg ttttcattca    975


ttaataataa tttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa   1035


ctctacagtc tcaaaatgac ctgataaatt gataagacaa agatgagatt attggggctg   1095


ttcatattat gattcagaat cattttctat tgtggtatta taggttggtt aaagtgatgg   1155
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cctttttgat gggttttgtt gtgtcttgtg aacaagtcgt tactgtgtcc attattggaa 1215

tggaattatc actactgtat catgagtggg tattttgatt ctatggttcc ctcagtatta 1275

catcttgact tgtaatcaat tatgaatatt tcttgatatt taatgtatag gacatttatt 1335

tatactcaat aaatattttt caaaagg   1362

<210> 63

<211> 622

<212> PRT

<213> Homo sapiens

<400> 63

Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro

1   5   10   15

Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly

            20   25   30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr

        35   40   45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg

    50   55   60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn

                65   70   75   80

Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val
                        85   90   95

Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp
                       100   105   110

Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser
                       115   120   125

Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp
           130   135   140

Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln Phe Gly His Thr
145   150   155   160

Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met
                       165   170   175

Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His
                       180   185   190

Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn
                       195   200   205

Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu
           210   215   220

Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn
225   230   235   240

Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys
                  245   250   255

Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln
                  260   265   270

Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp
            275   280   285

Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile
      290   295   300

Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile
305   310   315   320

Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser
                  325   330   335

Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile
                  340   345   350

Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe
      355   360   365

Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn
      370   375   380

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Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro
385   390   395   400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu
             405   410   415

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
             420   425   430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
             435   440   445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
             450   455   460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
465   470   475   480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
             485   490   495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
             500   505   510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
             515   520   525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
                              199/735

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        530                535                540
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Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg

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545                550                555                560
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Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe

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            565                570                575
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Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys

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            580                585                590
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Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr

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        595                600                605
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Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val

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    610                615                620
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<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(1879)

<400> 64

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                    Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala
                     1               5                   10


ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat    97
Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His
         15                  20                  25


tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat    145
Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp
         30                  35                  40


gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat    193
Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr
 45                  50                  55                  60


gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg    241
Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro
                 65                  70                  75


gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga    289
Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg
                 80                  85                  90


ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa    337
Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln
                 95                  100                 105


ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa    385
Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln
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                110   115   120

ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct   433
Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro
125   130   135   140

tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag   481
Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln
                   145   150   155

ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat   529
Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp
                   160   165   170

gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca   577
Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala
         175   180   185

tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat   625
Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn
         190   195   200

gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat   673
Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His
205   210   215   220

tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa   721
Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu
                   225   230   235

gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt   769
Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu
           240   245   250

gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa   817
Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln
           255   260   265

gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag   865
Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys
           270   275   280

ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct   913
Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro
285   290   295   300

ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat   961
Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp
           305   310   315

tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta   1009
Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val
           320   325   330

cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg   1057
Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu
           335   340   345

ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg   1105
Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp
    350   355   360

ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca   1153
Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro
365   370   375   380

ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg   1201
Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp
            385   390   395

aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag   1249
Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys
            400   405   410

aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc   1297
Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe
            415   420   425

tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt   1345
Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly
    430   435   440

gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg   1393
Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val
445   450   455   460

ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta   1441
                        204/735

Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu
    465   470   475

ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct 1489
Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser
    480   485   490

tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg 1537
Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp
    495   500   505

aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg 1585
Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met
    510   515   520

ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta tta ctc atg 1633
Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met
525   530   535   540

tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga 1681
Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg
    545   550   555

atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca acg tct att 1729
Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile
    560   565   570

gaa agc cca ttc aac cat gga tgt gta aga aat att ata gac ttc ttt 1777
Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe

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        575                   580                   585


gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc   1825
Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr
    590                   595                   600


agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag   1873
Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln
605                   610                   615                   620


ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtggtg cctgaaaatt     1929
Leu Val


gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989


tgtagggcta atggtgaatt ttacagtctt tttttcaaca cttttattaa caaaagtaaa 2049


catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109


ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct cacagtattt 2169


ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat cagaaatgtt 2229


cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc agtctagtac 2289


gagtattgca tctaattcca ggagcattgt tttaagttga ttgactagtt attatgtaca 2349


tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc tactgtgatg 2409
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ttgtcttcaa aggcaggaga aaataatgtt cacaataaaa tgtgctaaca atgttttgtt 2469

tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt gtagtaacct 2529

tactctgagg ttttacggtc tgataatgaa gcacttgcat gagtatagta agtcatgttt 2589

ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa tgtatactag 2649

cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagttccat 2709

ttttaagggt taaggtggta ttttcaagaa aaggcagaac aaataatgca aaattctcag 2769

taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata attgtagaca 2829

aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889

agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag tagaatttc 2948

<210> 65

<211> 632

<212> PRT

<213> Homo sapiens

<400> 65

Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp

1   5   10   15

Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu

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           20                    25                    30

Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly
        35                    40                    45


Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala
        50                    55                    60


Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly
    65                    70                    75                    80


Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp
                85                    90                    95


Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys
                100                   105                   110


Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu
                115                   120                   125


His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met
        130                   135                   140


Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys
145                   150                   155                   160


Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu
                165                   170                   175
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Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr
        180   185   190

Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg
        195   200   205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His
        210   215   220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val
225   230   235   240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile
        245   250   255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp
        260   265   270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn
        275   280   285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys
        290   295   300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile
305   310   315   320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly
        325   330   335

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His
        340   345   350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe
        355   360   365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe
        370   375   380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr
385   390   395   400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr
        405   410   415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser
        420   425   430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val
        435   440   445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp
        450   455   460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg
465   470   475   480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met

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                485                    490                    495


Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr
         500                    505                    510


Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser
         515                    520                    525


Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp
     530                    535                    540


Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly
545                    550                    555                    560


Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys
              565                    570                    575


Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg
         580                    585                    590


Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro
         595                    600                    605


Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile
         610                    615                    620


Ser Gly Ser Gly Tyr Gln Leu Val
625                    630
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<210> 66

<211> 4715

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (108)..(2003)

<400> 66

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cctccgcctc gcccgagccc cgggagggtg aaacgctttc tcccagc atg cag cgg   116

                                                    Met Gln Arg

                                                     1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat   164

Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp

       5   10   15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc   212

Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro

20   25   30   35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act   260

Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr

               40   45   50

cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat   308
His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr
            55   60   65

gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta   356
Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val
            70   75   80

cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc   404
Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile
          85   90   95

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att   452
Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile
100   105   110   115

gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc   500
Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala
           120   125   130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt   548
Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly
          135   140   145

gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg   596
Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu
          150   155   160

gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa   644

Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys
    165   170   175

gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg   692
Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met
180   185   190   195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta   740
Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu
            200   205   210

aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act   788
Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr
            215   220   225

gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt   836
Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu
            230   235   240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa   884
Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu
            245   250   255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac   932
Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn
260   265   270   275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc   980
His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe
                    214/735

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                    280                 285                 290

ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta     1028
Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu
            295                 300                 305


gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta     1076
Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu
            310                 315                 320


aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg     1124
Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp
        325                 330                 335


gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat     1172
Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His
340                 345                 350                 355


agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat     1220
Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr
            360                 365                 370


gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc     1268
Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile
            375                 380                 385


cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga     1316
His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly
            390                 395                 400
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aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa   1364
Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln
    405             410             415


aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc   1412
Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu
420             425             430             435


agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa   1460
Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys
            440             445             450


cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc   1508
His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys
            455             460             465


cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg   1556
Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met
            470             475             480


ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt   1604
Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly
    485             490             495


tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat   1652
Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp
500             505             510             515
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gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg       1700
Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met
                520                 525                 530


ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta       1748
Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val
                535                 540                 545


tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca       1796
Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr
                550                 555                 560


aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca       1844
Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr
                565                 570                 575


acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata       1892
Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile
580                 585                 590                 595


gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg       1940
Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val
                600                 605                 610


gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct       1988
Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser
                615                 620                 625


ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtggtg       2043
Gly Tyr Gln Leu Val
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Gly Tyr Gln Leu Val

630

cctgaaaatt gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga 2103

gcatgctatg tgtagggcta atggtgaatt ttacagtctt tttttcaaca cttttattaa 2163

caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

taattttaat ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct 2283

cacagtattt ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat 2343

cagaaatgtt cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc 2403

agtctagtac gagtattgca tctaattcca ggagcattgt tttaagttga ttgactagtt 2463

attatgtaca tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc 2523

tactgtgatg ttgtcttcaa aggcaggaga aaataatgtt cacaataaaa tgtgctaaca 2583

atgttttgtt tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt 2643

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agtcatgttt ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa 2763

tgtatactag cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa 2823

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acagttccat ttttaagggt taaggtggta ttttcaagaa aaggcagaac aaataatgca 2883

aaattctcag taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata 2943

attgtagaca aaataatggc atttaactaa agatggagca tgatctaagt acatagcaca 3003

tgtgaataaa agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag 3063

tagaatttca tccccaagag tatttcagtt tatccaatat tgagtaagtt ctgaaacagt 3123

tttagaaaaa attttctttt tgttaaatgt gatgcactga tcaatttttg tcacagcatt 3183

ttcatacctt catggtggac tactagtcac tgcttccata aatattgttt acagggtgag 3243

atttggttta ttcatcttaa gtgctgtagc aaactgtggt tcgagcaacc tgtgggaaat 3303

ctgtgagagg gaatggggtg ggagatgtgg gggaatggtg gtcagactga tgacagatcc 3363

tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctcttt 3423

gtgtctgtgt tagtgttttt aaagctgctc atttcatttt gtccaaccaa aaagaaaagg 3483

gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543

caagttcact gcatgtctga tgcttggtaa aactagtctt ccctgtaaaa tgcagattac 3603

aggtattaaa gcaatctagt ggtatacccg ccccttgcct tagtaagagg agcagtgaaa 3663

tgtatatagt tgatgttcag tatttccaag taccattttt atatagtagc ttatttgacc 3723
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ataagtcaca catcaaaaaa agattaccct tagtgtatgt gttttaatat tagaaaattg 3783

gcatatgtac tttatttttg aaaagggaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccattttgtc atagaatgta aaaattggtt aactttacaa atgtcagcta gttttgacta 3903

ctaattgggg gaaattttag ataatttta aattcaaagt tatttataaa atgctagaat 3963

ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc atttttatcg 4023

aatacatttt tatcaacagt taaagactat ggtggttttt tcagagtttg gctaagaatg 4083

ttgttaccat cttctttgtt tgtggtacaa tattttcagt gcaaaagaga tgtcattcag 4143

ttaaaaagac aaacctctag atgtgtaatt acatggaaaa tactagcaat gtgaatgctt 4203

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ggagccagct atgcagcagt ataccatctg tttaattatt ttgtaggtcc tgtgtgtgga 4323

accaactata aacccagttc taaagttgtg tatgatggtg aacctttggg aatagttctt 4383

atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443

tacttccttg gagttttttt tcattcatat ttttgttgtt tccaggaatt tatttgatat 4503

taatgggcgt aaaacagcat cattgtactt aagctatgga tgtttttatt ttatattttc 4563

tttatttata actgtgccaa gtattatttt gctacttacc gtgttattct gtggaaagaa 4623

aaacctgtaa agtgtttaat aaattagccc tccttacata aattaaatgt caaaattttg 4683

taaaatatta atcagaataa atactgactc tt   4715

<210> 67

<211> 498

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu
1   5   10   15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
            20   25   30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
        35   40   45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
    50   55   60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
65   70   75   80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

```
                  85                    90                    95


Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
            100                   105                   110


Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
            115                   120                   125


Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
            130                   135                   140


Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
145                   150                   155                   160


Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
                  165                   170                   175


Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
                  180                   185                   190


Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
            195                   200                   205


Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
            210                   215                   220


Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
225                   230                   235                   240
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Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
          245   250   255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
          260   265   270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
          275   280   285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
          290   295   300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305   310   315   320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
          325   330   335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
          340   345   350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
          355   360   365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
          370   375   380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385   390   395   400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
            405   410   415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
            420   425   430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
            435   440   445

Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln
        450   455   460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465   470   475   480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
                485   490   495

Ser Cys

<210> 68

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 68

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct   51

                 Met Ala Arg Leu Glu Val Ile Glu Leu Pro

                  1   5   10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac   99

His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His

            15   20   25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att   147

Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

            30   35   40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg   195

Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val

            45   50   55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc   243

His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly

          60   65   70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa   291

Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu

  75   80   85   90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct   339

Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
          95   100   105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg   387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
           110   115   120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag   435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
           125   130   135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc   483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
          140   145   150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac   531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
155   160   165   170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag   579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
           175   180   185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg   627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val
           190   195   200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg   675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val

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                   205   210   215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct   723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
        220   225   230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg   771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
235   240   245   250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc   819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala
                   255   260   265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag   867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
               270   275   280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac   915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
               285   290   295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca   963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro
        300   305   310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc   1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
315   320   325   330
</pre>

```
aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc      1059
Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly
            335                 340                 345


tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg      1107
Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr
            350                 355                 360


cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca      1155
His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser
            365                 370                 375


tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc      1203
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly
            380                 385                 390


act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac      1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp
395                 400                 405                 410


ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc      1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg
            415                 420                 425


tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc      1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
            430                 435                 440
```

```
tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta      1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu
        445                 450                 455


cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca      1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
        460                 465                 470


aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc      1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
475                 480                 485                 490


cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat     1545
Gln Lys Leu Trp Glu Phe Ser Cys
                495


aaagaattca tatcatctgt taatggcgac agtttttgtt tcttcctttg aatttttat    1605


attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg   1665


gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt   1725


cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt   1785


aggcttttta aaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg     1845


atttcctagg agttggtttt tttttttta aagcataaat aaatttaatt gcatcag        1902
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229/735

<210> 69

<211> 498

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu
1   5   10   15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
                20   25   30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
                35   40   45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
        50   55   60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
65   70   75   80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
                85   90   95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
                100   105   110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
                115   120   125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
     130   135   140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
145   150   155   160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
          165   170   175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
          180   185   190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
          195   200   205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
          210   215   220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
225   230   235   240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
          245   250   255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
          260   265   270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
               231/735

                275   280   285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
   290   295   300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305   310   315   320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
                325   330   335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
                340   345   350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
                355   360   365

Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
   370   375   380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385   390   395   400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
                405   410   415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
                420   425   430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
        435   440   445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln
        450   455   460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465   470   475   480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
                485   490   495

Ser Cys

<210> 70

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 70

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct   51

                        Met Ala Arg Leu Glu Val Ile Glu Leu Pro
                        1   5   10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac   99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
                15   20   25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att   147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
                30   35   40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg   195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
                45   50   55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc   243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
     60   65   70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa   291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
75   80   85   90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct   339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
                95   100   105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg   387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
             110   115   120

```
act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag      435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
        125              130              135


cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc      483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
        140              145              150


ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac      531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
155              160              165              170


tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag      579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
                175              180              185


gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg      627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val
        190              195              200


acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg      675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val
        205              210              215


cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct      723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
        220              225              230


ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg      771
```

```
    Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
    235             240             245             250


    gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc    819
    Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala
                    255             260             265


    cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag    867
    Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
                    270             275             280


    ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac    915
    Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
                285             290             295


    ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca    963
    Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro
            300             305             310


    gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc    1011
    Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
    315             320             325             330


    aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc    1059
    Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly
                    335             340             345


    tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg    1107
    Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr
```

236/735

                350   355   360

cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca   1155
His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser
         365   370   375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc   1203
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly
     380   385   390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac   1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp
395   400   405   410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc   1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg
                415   420   425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc   1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
         430   435   440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta   1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu
         445·   450   455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca   1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
     460   465   470

```
aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc     1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
475             480             485             490


cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat     1545
Gln Lys Leu Trp Glu Phe Ser Cys
            495


aaagaattca tatcatctgt taatggcgac agttttgtt tcttcctttg aatttttat      1605


attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg     1665


gctaaagcgt cttctatcat atcgaattgg dacaatgata gaagacaatc tttgttttgt     1725


cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt      1785


aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg      1845


atttcctagg agttggtttt tttttttta aagcataaat aaatttaatt gcatcag          1902
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<210> 71

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His

```
            1                 5                 10                15

Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
                20                25                30

Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
                35                40                45

Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
             50                55                60

Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
65                70                75                80

Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
                   85                90                95

Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp
                  100               105               110

Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr
                  115               120               125

Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala
                  130               135               140

Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu
145               150               155               160
```

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
            165   170   175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly
            180   185   190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val
            195   200   205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg
        210   215   220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly
225   230   235   240

Gln Trp Ile Gln Arg
            245

<210> 72

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (127)..(861)

<400> 72

ggaagtcggc caccttcctc cgtcccggcc gttagcccag ccaagcccag ccaagcccag 60

ccaagccccg ccgatcgcgg gcaccggagc cagccccgca gcgggtcccg cctgtctgtc 120

```
acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct      168
       Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser
        1               5                   10
```

```
atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc     216
Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser
 15              20                  25                  30
```

```
atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc     264
Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile
                35                  40                  45
```

```
ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac     312
Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His
            50                  55                  60
```

```
cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg     360
Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg
            65                  70                  75
```

```
ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct     408
Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser
 80                  85                  90
```

```
ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc     456
```

```
              Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile
               95              100             105             110


              gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc    504
              Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe
                              115             120             125


              agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag    552
              Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys
                          130             135             140


              gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg    600
              Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu
                      145             150             155


              gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat    648
              Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn
                  160             165             170


              ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc    696
              Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile
              175             180             185             190


              gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc    744
              Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly
                              195             200             205


              acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att    792
              Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile
```

242/735

210   215   220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt   840
Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val
         225   230   235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact   891
Leu Gly Gln Trp Ile Gln Arg
         240   245

gtcagaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951

ctagggtctg tgaacgaggc ctgtctcttc cctggggttt ctttccatgg cctttatttc 1011

tcctcttcca gtgggagttt tgcaggctct tctctgtgga aacttcacga gcgttggctg 1071

ggcctcggct tcgctggagt gtactccagg gtgaaggcag agtgggattt gagacccagg 1131

tagtggagga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191

tcaccgggca tagcctggaa gccccaagtc tgttctgact ttgcctggct gtctccttga 1251

cccgcctcct agatcattgt ccttgatgtc caggctgggt catttaaaat agagatgcaa 1311

tcaggaaggt tggggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371

tcagcacctg agtcacagcc caggtgcccg gaagcagcct cttcgcatag gcagtgattt 1431

gcgattactt taaagctcac cttttttctt cccctctctg ttcgctgctg tcagcataat 1491

243/735

gattgtgttc cttccctatg ggatccatct gttttgtaaa caataaagcg tctgagggag 1551

<210> 73

<211> 352

<212> PRT

<213> Homo sapiens

<400> 73

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

1   5   10   15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

            20   25   30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

        35   40   45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

    50   55   60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65   70   75   80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu

            85   90   95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp

```
                    100                   105                      110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
          115                   120                   125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
          130                   135                   140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145                   150                   15b                   160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
                    165                   170                   175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
                    180                   185                   190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
                    195                   200                   205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
          210                   215                   220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225                   230                   235                   240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
                    245                   250                   255
```

```
Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
            260                 265                 270


Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
            275                 280                 285


Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
            290                 295                 300


Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305                 310                 315                 320


Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
                325                 330                 335


Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
                340                 345                 350
```

<210> 74

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 74

ttaggccggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc 60

tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga   114
                                            Met Glu Ser Gly
                                             1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg   162
Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
 5   10   15   20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc   210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
                    25   30   35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag   258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
                40   45   50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata   306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
                55   60   65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg   354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
         70   75   80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag   402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
 85   90   95   100

247/735

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc   450

Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile

              105   110   115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag   498

Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

              120   125   130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg   546

Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val

              135   140   145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag   594

Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln

             150   155   160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa   642

Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys

165   170   175   180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca   690

Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr

             185   190   195

ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg   738

Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro

             200   205   210

ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc   786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
        215   220   225

ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg   834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
        230   235   240

ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg   882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
245   250   255   260

aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag   930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
                265   270   275

gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct   978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
            280   285   290

gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc   1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
        295   300   305

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc   1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
        310   315   320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga   1122
                              249/735

```
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg
325                 330                 335                 340
```

```
cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg          1168
Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
                    345                 350
```

```
gaagccgcac agcttgacct ggaagcaccc ctgcccctt ttcagggatt tttatctcga   1228

ggcctttgga ggagcagtgg tggggtagc tgtcacctcc aggtatgatt gagggaggaa   1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga   1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg   1408

tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac   1468

caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgttttttc tggtgaatcg    1528

ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca   1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc   1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc   1708

tttcccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag   1768

tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag   1828
```

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agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctcgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc ccctcccagt attaccattt gcccctcacc tgcccttggt 2188

gagccttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctctttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc   2401

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
1   5   10   15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
              20   25   30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
              35   40   45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
              50   55   60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65   70   75   80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
                  85   90   95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
                  100   105   110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
                  115   120   125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
              130   135   140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145   150   155   160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
                              252/735

                165   170   175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
            180   185   190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
            195   200   205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
        210   215   220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225   230   235   240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
                245   250   255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
                260   265   270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
            275   280   285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
            290   295   300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305   310   315   320

```
    Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
                325                 330                 335


    Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
                340                 345                 350
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<210> 76

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 76

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ttaggccggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc  60


tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga     114
                                                Met Glu Ser Gly
                                                  1


ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg   162
Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
  5                 10                  15                  20


gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc   210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
```

```
                  25                  30                  35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag    258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
              40                  45                  50


agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata    306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
              55                  60                  65


gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg    354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
          70                  75                  80


gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag    402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
      85                  90                  95                  100


atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc    450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
              105                 110                 115


att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag    498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
              120                 125                 130


gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg    546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
          135                 140                 145
```

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```
gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag    594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
    150             155             160


tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa    642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
165             170             175             180


ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca    690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
            185             190             195


ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg    738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
            200             205             210


ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc    786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
            215             220             225


ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg    834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
    230             235             240


ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg    882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
245             250             255             260
```

```
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag      930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
            265                 270                 275


gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct      978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
            280                 285                 290


gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc     1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
            295                 300                 305


ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc     1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
            310                 315                 320


gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga     1122
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg
325                 330                 335                 340


cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg          1168
Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
            345                 350


gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228


ggcctttgga ggagcagtgg tggggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288


tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348
```

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468

caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgttttttc tggtgaatcg 1528

ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc 1708

tttcccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctcgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc ccctcccagt attaccattt gcccctcacc tgcccttggt 2188

gagcctttta gtgcaagaca datggggctg ttttcccca cctctgagta gttggaggtc 2248

acatacacag ctctttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc   2401

<210> 77

<211> 697

<212> PRT

<213> Homo sapiens

<400> 77

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala
 1   5   10   15

Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser
                20   25   30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile
            35   40   45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile
        50   55   60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile
65   70   75   80

Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn
                85   90   95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser
               100   105   110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu
               115   120   125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser
       130   135   140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu
145   150   155   160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys
               165   170   175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile
               180   185   190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe
               195   200   205

Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile
210   215   220

Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp
                              260/735

```
      225                    230                    235                    240
```

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu
```
               245                    250                    255
```

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met
```
               260                    265                    270
```

Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr
```
               275                    280                    285
```

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe
```
               290                    295                    300
```

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His
```
     305                    310                    315                    320
```

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp
```
               325                    330                    335
```

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe
```
               340                    345                    350
```

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala
```
               355                    360                    365
```

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser
```
               370                    375                    380
```

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe
385   390   395   400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile
              405   410   415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu
              420   425   430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu
              435   440   445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly
       450   455   460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys
465   470   475   480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp
              485   490   495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp
              500   505   510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp
       515   520   525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu
       530   535   540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn
545   550   555   560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp
           565   570   575

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp
           580   585   590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys
           595   600   605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp
           610   615   620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met
625   630   635   640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp
           645   650   655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys
           660   665   670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr
           675   680   685

Gly Gln Gly Phe Lys Leu Val Lys Ser
                    263/735

<210> 78

<211> 3008

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (372)..(2462)

<400> 78

cgtaccgtcg cggatttcgg cggcggaaac atggcggtcg cggccgggcc ggtaacggag 60

aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aattttgta acgtgaggga aaagcccaca 360

ttgctggtta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc 410
            Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu
            1   5   10

```
tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg      458
Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met
    15                  20                  25


cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg      506
His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu
    30                  35                  40                  45


gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat      554
Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn
                    50                  55                  60


tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc      602
Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile
                    65                  70                  75


gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt      650
Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser
                    80                  85                  90


ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt      698
Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu
                    95                  100                 105


gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat      746
Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr
110                 115                 120                 125


ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag      794
```

265/735

Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu
              130   135   140

aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt   842
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val
              145   150   155

gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg   890
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu
              160   165   170

gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg   938
Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met
         175   180   185

ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta   986
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu
190   195   200   205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa   1034
Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys
              210   215   220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct   1082
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro
              225   230   235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa   1130
Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys
                         266/735

```
                240                      245                      250

ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt    1178
Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe
    255                      260                      265


gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt    1226
Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu
270                      275                      280                      285


aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt    1274
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe
                290                      295                      300


gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg    1322
Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp
            305                      310                      315


gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac    1370
Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His
            320                      325                      330


agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg    1418
Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met
    335                      340                      345


cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt    1466
Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu
350                      355                      360                      365
```

267/735

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att   1514
Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile
                370   375   380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat   1562
Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His
                385   390   395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga   1610
Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly
                400   405   410

tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca   1658
Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro
        415   420   425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act   1706
Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr
430   435   440   445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag   1754
Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu
                450   455   460

acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg   1802
Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu
        465   470   475

```
cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc      1850
His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro
         480                 485                 490


aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca      1898
Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr
         495                 500                 505


gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt      1946
Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu
510                 515                 520                 525


ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att      1994
Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile
                    530                 535                 540


atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg      2042
Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg
                    545                 550                 555


aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa      2090
Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys
                    560                 565                 570


aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca      2138
Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr
         575                 580                 585


aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg      2186
```

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```
Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp
590              595              600              605


act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg     2234
Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg
             610              615              620


tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag     2282
Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
             625              630              635


cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg     2330
His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
             640              645              650


gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt     2378
Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
     655              660              665


ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg     2426
Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val
670              675              680              685


ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac          2472
Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
             690              695


cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532
```

gtatgctgta tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg 2592

tcttttctta agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa 2652

gtatgtaggg agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712

ctttcaggaa tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa 2772

tggtcaatga tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat 2832

gtagaccaga taaatttgtt tactgtttta agaaaactac cagtttactt acagaagatt 2892

cttttttcca aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct 2952

tagaaaagaa agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac   3008

<210> 79

<211> 611

<212> PRT

<213> Homo sapiens

<400> 79

Met Glu Ala Ala Ser Leu Ser Leu Ser Asn Leu Trp Phe Gly Phe Leu
1   5   10   15

Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val
                20   25   30

Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg
       35   40   45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg
       50   55   60

Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala
65   70   75   80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu
             85   90   95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser
            100   105   110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe
            115   120   125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe
            130   135   140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu
145   150   155   160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys
            165   170   175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe
            180   185   190

Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val
    195   200   205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile
    210   215   220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys
225   230   235   240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg
                245   250   255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln
                260   265   270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser
                275   280   285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
    290   295   300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
305   310   315   320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe
                325   330   335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln
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                340                    345                    350

Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe
        355                    360                    365


Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser
        370                    375                    380


Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu
385                    390                    395                    400


Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr
                405                    410                    415


Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp
                420                    425                    430


Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly
        435                    440                    445


Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr
        450                    455                    460


Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val
465                    470                    475                    480


Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro
                485                    490                    495
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Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn
500   505   510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala
        515   520   525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro
    530   535   540

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile
545   550   555   560

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu
                565   570   575

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met
            580   585   590

Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu
        595   600   605

Val Lys Ser
    610

<210> 80

<211> 3007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (629)..(2461)

<400> 80

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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta catgtgtaaa tcactgcgtt attgctttag tcattgtctc tatttagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggtatcttg 480

ctatttagcc agaatcaatt tattggttgc tatatgctta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc   652
                                  Met Glu Ala Ala Ser Leu Ser Leu
                                  1   5

```
tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat    700
Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp
        10              15              20
```

```
aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg    748
Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu
    25              30              35              40
```

```
ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga    796
Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg
                45              50              55
```

```
att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa    844
Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu
                60              65              70
```

```
ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg    892
Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val
            75              80              85
```

```
gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg    940
Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu
        90              95              100
```

```
att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt    988
Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val
105             110             115             120
```

att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat   1036
Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn
                125   130   135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc   1084
Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe
            140   145   150

ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc   1132
Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro
            155   160   165

ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct   1180
Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala
        170   175   180

gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga   1228
Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg
185   190   195   200

gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga   1276
Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly
                205   210   215

att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga   1324
Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly
            220   225   230

ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg   1372

```
        Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg
                  235               240               245


        aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc    1420
        Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg
                  250               255               260


        cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca    1468
        His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala
        265               270               275               280


        aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc    1516
        Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe
                            285               290               295


        ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg    1564
        Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly
                  300               305               310


        ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat    1612
        Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr
                  315               320               325


        gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca    1660
        Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr
                  330               335               340


        ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc    1708
        Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly
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              345                    350                    355                    360


          atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc   1756
          Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr
                       365                    370                    375


          tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat   1804
          Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His
                       380                    385                    390


          tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga   1852
          Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg
                  395                    400                    405


          cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga   1900
          His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly
                  410                    415                    420


          gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata   1948
          Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile
          425                    430                    435                    440


          gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc   1996
          Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile
                       445                    450                    455


          gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa   2044
          Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys
                  460                    465                    470
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att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca   2092
Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr
        475   480   485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa   2140
Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys
        490   495   500

gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act   2188
Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr
505   510   515   520

gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg   2236
Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp
            525   530   535

agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac   2284
Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His
            540   545   550

tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca   2332
Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala
            555   560   565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt   2380
Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe
        570   575   580

```
agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg    2428
Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu
585                590                595                600


gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg  2481
Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
                 605                610


gatattaata agcactcata ctaccaatta tcactaactt gccatttttt gtatgctgta  2541


tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg tcttttctta  2601


agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa gtatgtaggg  2661


agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa  2721


tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa tggtcaatga  2781


tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat gtagaccaga  2841


taaatttgtt tactgtttta agaaaactac cagtttactt acagaagatt cttttttcca  2901


aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct tagaaaagaa  2961


agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac                 3007
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<210> 81

<211> 184

<212> PRT

<213> Homo sapiens

<400> 81

Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu
1   5   10   15

Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln
                20   25   30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys
                35   40   45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln
            50   55   60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser
65   70   75   80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu
                85   90   95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro
                100   105   110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys
                115   120   125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser

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                130   135   140

Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile

145   150   155   160

Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro

                        165   170   175

Thr Glu Met Asp Glu Asn Glu Ser

                        180

<210> 82

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (285)..(836)

<400> 82

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gcgcgcgcgg gagcgcggga ggatcggcgg ctcgcggtca ctggtccctg gctcggttcc 120

ccgcacccCg gggctcacac ttacccgcgc ggaggagcag cggccgggtg tccacccCca 180

tcctgcgccc agtctcctcg attcccctcg ctctgagccg ggagagccga acagctgaag 240

```
agagttcact gactccccag ccccaggtgg gccttgtgca catc atg acc agt ttt   296
                                                    Met Thr Ser Phe
                                                     1


gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt   344
Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val
 5                  10                  15                  20


tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt   392
Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe
                    25                  30                  35


aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat   440
Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn
                    40                  45                  50


tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt   488
Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val
                    55                  60                  65


cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc   536
Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser
                    70                  75                  80


ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc   584
Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser
 85                  90                  95                  100
```

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```
aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg     632
Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met
                105                 110                 115


gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag     680
Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu
            120                 125                 130


tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc     728
Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu
            135                 140                 145


ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc     776
Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly
        150                 155                 160


act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat     824
Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp
165                 170                 175                 180


gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa         876
Glu Asn Glu Ser


gagctctgta gatgctgtat agacactaaa taagagttga ttagggtagt atattatagt 936


catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaattgtg 996


ttagtcatta acttagtcac ctgttgtatt ctggatctac acaaaattat tttaactgct 1056
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cttattaatc tgtgaggatt aatatacaaa aagtatcctt tgagatgaag tcgtgttctc 1116

aaaataaggt tatattattt tctttttctg cttgattttc atcttgtgtt ttgctttgtt 1176

tttgtaagga accatctctt ggtttggtca catcagttca caacagccat ttgttttcaa 1236

ggtcaaggct ccaggcaggt tgttactggt gtttgcagcc tgtcagtact tgcagtactg 1296

gaataggttc taggctagtg tctgcgcgtc actgtggttt tagcatggga ggacttattt 1356

gagaaatact accttacttt tctatgattt cttttacag agttatagtg tgtttactcc 1416

taagatgaca gttctctttg tctatattca gcatctaaga caaatattta aacattttaa 1476

agaaccactg tgttaagttt aggattattt acttaccaaa ttagaagttt gacttttatg 1536

tgttatacac aatcttaaaa tttcacgaat tcaccttttt aatagtatcc atgtacataa 1596

taaaatcaaa gtttaattag c                                          1617
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<210> 83

<211> 392

<212> PRT

<213> Homo sapiens

<400> 83

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Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
1               5                   10                  15
```

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
            20   25   30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
            35   40   45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
         50   55   60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65   70   75   80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
                  85   90   95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
            100   105   110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
            115   120   125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
            130   135   140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145   150   155   160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

                    165   170   175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
                    180   185   190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
                    195   200   205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
                    210   215   220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225   230   235   240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                    245   250   255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
                    260   265   270

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
                    275   280   285

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
                    290   295   300

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
305   310   315   320

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
                325   330   335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
                340   345   350

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
                355   360   365

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
    370   375   380

Val Glu Ser Pro Val Gln Lys Val
385   390

<210> 84

<211> 1898

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1294)

<400> 84

acttccgctg gccgctggct cgctggccgc tcctggaggc ggcggcggga gcgcaggggg 60

cgcgcggccc ggggactcgc attccccggt tcccctcca ccccacgcgg cctggacc 118

```
atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc    166
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1               5                  10                 15


cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc    214
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
                20                 25                 30


cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc    262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
            35                 40                 45


ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac    310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
        50                 55                 60


tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt    358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65                 70                 75                 80


gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc    406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
                85                 90                 95


cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg    454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
                100                105                110
```

```
ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg      502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
        115                 120                 125


ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca      550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
        130                 135                 140


ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga      598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145                 150                 155                 160


gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag      646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
                165                 170                 175


ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc      694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
                180                 185                 190


aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc      742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
                195                 200                 205


ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg      790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
        210                 215                 220


ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac      838
```

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225   230   235   240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc   886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                  245   250   255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc   934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
                  260   265   270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc   982
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
                  275   280   285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc   1030
Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
                  290   295   300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg   1078
Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
305   310   315   320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc   1126
Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
                  325   330   335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg   1174
Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
                        293/735

```
                  340                     345                     350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga   1222
Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
              355                     360                     365


gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct   1270
Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
              370                     375                     380


gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt   1324
Val Glu Ser Pro Val Gln Lys Val
385                     390


gaaataggac cctcccacca tccccttctg ctgtaacctc tgagggagct ggctgaaagg   1384


gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc   1444


ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agtttattct   1504


gagccccggg ggtagacagt cctcagtgag gggttttggg gagtttgggg tcaagagagc   1564


ataggtaggt tccacagtta ctcttcccac aagttccctt aagtcttgcc ctagctgtgc   1624


tctgccacct tccagactca ctcccctctg caaatacctg catttcttac cctggtgaga   1684


aaagcacaag cggtgtaggc tccaatgctg ctttcccagg agggtgaaga tggtgctgtg   1744


ctgaggaaag gggatgcaga gccctgccca gcaccaccac ctcctatgct cctggatccc   1804
```

taggctctgt tccatgagcc tgttgcaggt tttggtactt tagaaatgta acttttttgct 1864

cttataattt tattttatta aattaaatta ctgc   1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
1   5   10   15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
                20   25   30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
            35   40   45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
        50   55   60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65   70   75   80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
                85   90   95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
                100   105   110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
                115   120   125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
            130   135   140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145   150   155   160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
                165   170   175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
                180   185   190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
            195   200   205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
        210   215   220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225   230   235   240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                                296/735

```
                   245                  250                  255

      Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
                   260                  265                  270


      Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
                   275                  280                  285


      Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
                   290                  295                  300


      Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
      305                  310                  315                  320


      Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
                   325                  330                  335


      Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
                   340                  345                  350


      Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
                   355                  360                  365


      Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
                   370                  375                  380


      Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
      385                  390                  395                  400
```

```
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
            405                 410                 415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
            420                 425                 430
```

<210> 86

<211> 2018

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1414)

<400> 86

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acttccgctg gccgctggct cgctggccgc tcctggaggc ggcggcggga gcgcaggggg 60

cgcgcggccc ggggactcgc attccccggt tcccctcca ccccacgcgg cctggacc    118
```

```
atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc    166
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1               5                  10                  15
```

```
cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc    214
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
            20                  25                  30
```

```
cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc    262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
         35                  40                  45
```

```
ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac    310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
         50                  55                  60
```

```
tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt    358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65                  70                  75                  80
```

```
gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc    406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
                 85                  90                  95
```

```
cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg    454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
                100                 105                 110
```

```
ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg    502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
        115                 120                 125
```

```
ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca    550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
        130                 135                 140
```

```
ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga    598
```

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145   150   155   160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag   646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
              165   170   175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc   694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
              180   185   190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc   742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
              195   200   205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg   790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
      210   215   220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac   838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225   230   235   240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc   886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
              245   250   255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc   934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

```
                260                  265                  270


atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg    982
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
        275                  280                  285


cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt   1030
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
        290                  295                  300


ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa   1078
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305                  310                  315                  320


cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag   1126
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
                325                  330                  335


ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag   1174
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
        340                  345                  350


ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc   1222
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
        355                  360                  365


atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt   1270
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
370                  375                  380
```

```
ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg    1318
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385             390             395             400
```

```
gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag    1366
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
                405             410             415
```

```
caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt    1414
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
                420             425             430
```

```
tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tccccttctg 1474

ctgtaacctc tgagggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca 1534

gaccagctct gcagcagggg attggggagc ccaggaggca gccttccctt ttgccttaag 1594

tcacccatct tccagtaagc agtttattct gagccccggg ggtagacagt cctcagtgag 1654

gggttttggg gagtttgggg tcaagagagc ataggtaggt tccacagtta ctcttcccac 1714

aagttccctt aagtcttgcc ctagctgtgc tctgccacct tccagactca ctcccctctg 1774

caaatacctg catttcttac cctggtgaga aaagcacaag cggtgtaggc tccaatgctg 1834

ctttcccagg agggtgaaga tggtgctgtg ctgaggaaag gggatgcaga gccctgccca 1894
```

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gcaccaccac ctcctatgct cctggatccc taggctctgt tccatgagcc tgttgcaggt 1954

tttggtactt tagaaatgta acttttgct cttataattt tattttatta aattaaatta 2014

ctgc 2018

<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser
1   5   10   15

Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser
            20   25   30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His
            35   40   45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser
        50   55   60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys
65   70   75   80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val

                    85   90   95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe
              100   105   110

Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala
              115   120   125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu
              130   135   140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser
145   150   155   160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu
                    165   170   175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile
              180   185   190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg
              195   200   205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu
              210   215   220

Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala
225   230   235

<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (111)..(815)

<400> 88

aaaaggaaga cagaaaagcc gcgggctgac tgtggtggcg ctcgcctgca gattgaaaag 60

aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt   116
                                                             Met Gly
                                                              1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt   164
Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly
              5   10   15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc   212
Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser
         20   25   30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat   260
Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn
35   40   45   50

```
aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa    308
Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu
                55                  60                  65


gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg    356
Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val
            70                  75                  80


ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat    404
Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn
        85                  90                  95


ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag    452
Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu
        100                 105                 110


atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat    500
Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn
115                 120                 125                 130


ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat    548
Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp
                135                 140                 145


act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac    596
Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn
                150                 155                 160


agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat    644
```

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Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn
        165   170   175

ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc   692
Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala
        180   185   190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt   740
Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe
195   200   205   210

cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga   788
Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg
            215   220   225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat   835
Asn Met Val Gln Arg Gln Phe Ile Ala
            230   235

gtggctggct cttgttttgt aaaccaaatg attaatcttc acttgagaaa gcagtttcta 895

ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955

taaatttctg caggacagcc tataaaattg tggtactttt tgatgtttca gtaaacttga 1015

cattgtcaga gtttcaagga cttttctttc acaattttcc tagttcatgg atatgaaaaa 1075

ggaattctca atccatattc cttgtattga accttgaaca aaaacttgta tgacagacat 1135

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ttttaaaaat gtgacaacac ttttattctc tgaatttga tctcaaagga cacagaaaaa 1195

aaatggcccc aggagatctg atcacacttc ctcctgaggc acctctcatg gatgttgcaa 1255

taagcattcg ggtactatca cccagaaata tgaattgcca gaatagaaca tttagcatgt 1315

taagcgttga tgcatataaa atcagaaata gatgtgagaa tggtggaact ttttaaaaga 1375

acccagtcaa atgtattttc tgctgaaatc tgcatatttg gaggcatttc ccaccaccga 1435

ttcacagccc atttgatagt gtggtagtta gggacttcgt ggagtggtgt tcagacgtcc 1495

cctggggctt aaatctcttc atattagtca tcatttgtaa ctatggcttt atttgcagag 1555

cttctaaaag gcgtataact gtgtgagtgg ccagatattc actttttaga tcaaaaacct 1615

ctcttatgga agctttaaaa gtttccgtca cacacaattc tcttctcagg aagtatttct 1675

catttaggtc ttcaaagtag cctgactgtg tgcatgtgtg tgtgtgatag gttatttata 1735

aagactttgg atagaaggag atgtatttta ttacctccta ttctagagcc ccatgctcct 1795

aacaagccag agaggcccca aacaggattg tttctttcct ccacagccct tctgcccatc 1855

tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggtcatgtc 1915

atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgcca 1975

ctgaggatga atgtaactgt gggcaaacta tttaccctcc tttatctgtg aaatgaaagg 2035

```
gttgaattga tggatctcta aaggctttg tcctctatga ggatgtgaaa aactagggac 2095


cacaaaaggg aacaagcaaa aaagtttgga ttcgataaag tgatatgtaa tagttgcaga 2155


aggctttata tatgcttata atgaaaagat attttttgta tattgacagc ataatttatt 2215


tttaatgctg tcattacact taaagtcaca ggaaaaaaat atacatgctt actcaggctt 2275


tcttaaaaat aaattttat agagatcctt gagtaaagac attttgctta atttcttttt 2335


tcttattccc cacttgtata tcccctacca gtaccgggat ctgcacacat cttttttgcag 2395


ttacctcttc atagccatga accaaaacgt tctatgagga gcatgcaagt aagtcaagcc 2455


tcctattctg ttagtactta ttagaggagg agatggtttt cattgcatag tgacattttc 2515


ttagccttaa cgttctgata gtagcttact actcacttct ctttttcagt tttcataata 2575


agtattcatt tttttgccat aatgcttcct gtaaagccaa ttttatatac taataaaaca 2635


tgaactgccc actcttcatg cctgccaaac ttggggcaat tgatgctaaa tggtattttt 2695


aaaataaatg ttttttattct tt                                        2717
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<210> 89

<211> 245

<212> PRT

<213> Homo sapiens

<400> 89

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
1   5   10   15

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
            20   25   30

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
            35   40   45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
        50   55   60

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
65   70   75   80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
                85   90   95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
            100   105   110

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
        115   120   125

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
        130   135   140

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Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
145   150   155   160

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
                165   170   175

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
                180   185   190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
                195   200   205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
        210   215   220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225   230   235   240

Gln Tyr Glu Ile Val
                245

<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (60)..(794)

<400> 90

gcgtctcgct ctctgtgttc caatcgcccg gtgcggtggt gcagggtctc gggctagtc 59

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atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt   107
Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
 1               5                  10                  15

ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc   155
Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
                20                  25                  30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat   203
Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
                35                  40                  45

tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc   251
Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
        50                  55                  60

att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt   299
Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
65                  70                  75                  80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt   347
Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
                85                  90                  95
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ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt      395
Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
            100             105             110


gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag      443
Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
            115             120             125


gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta      491
Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
            130             135             140


gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga      539
Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
145             150             155             160


gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt      587
Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
            165             170             175


tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta      635
Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
            180             185             190


aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa      683
Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
            195             200             205
```

```
atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg    731
Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
     210             215             220


att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac    779
Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225             230             235             240


cag tat gag ata gtg taacccaatg tatctgtggg cctattcctc tctaccttta    834
Gln Tyr Glu Ile Val
                245


aggacattta gggtcccccc tgtgaattag aaagttgctt ggctggagaa ctgacaacac 894


tacttactga tagaccaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga 954


cctaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca 1014


atcaagatgt atgtttgcta tgttctaagt ccaccttcta tcccattcat gttagatcgt 1074


tgaaaccctg tatccctctg aaacactgga gagctagta aattgtaaat gaagtaatac 1134


tgtgttcctc ttgactgtta tttttcttag taggggcct ttggaaggca ctgtgaattt 1194


gctattttga tgtagtgtta caagatggaa aattgattcc tctgactttg ctattgatgt 1254


agtgtgatag aaaattcacc cctctgaact ggctccttcc cagtcaaggt tatctggttt 1314


gattgtataa tttgcaccaa gaagttaaaa tgttttatga ctctctgttc tgctgacagg 1374
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cagagagtca cattgtgtaa tttaatttca gtcagtcaat agatggcatc cctcatcagg 1434

gttgccagat ggtgataaca gtgtaaggcc ttgggtctaa ggcatccacg actggaaggg 1494

actactgatg ttctgtgata catcaggttt cagcacacaa cttacatttc tttgcctcca 1554

aattgaggca tttattatga tgttcatact ttccctcttg tttgaaagtt tctaattatt 1614

aaatggtgtc ggaattgttg tattttcctt aggaattcag tggaacttat cttcattaaa 1674

tttagctggt accaggttga tatgacttgt caatattatg gtcaacttta agtcttagtt 1734

ttcgtttgtg cctttgatta ataagtataa ctcttataca ataaatactg ctttcctct 1793

<210> 91

<211> 180

<212> PRT

<213> Homo sapiens

<400> 91

Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
1   5   10   15

Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
                20   25   30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
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```
                35                    40                          45

      Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
             50                    55                    60

      Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
             65                    70                    75              80

      Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
                     85                    90                    95

      Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
                     100                   105                   110

      Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
                 115                   120                   125

      Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
             130                   135                   140

      Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
      145                   150                   155                   160

      Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
                     165                   170                   175

      Ala Leu Leu Gln
                 180
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<210> 92

<211> 970

<212> DNA ·

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(565)

<400> 92

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tttttcagct aaaggggaga tctgg atg gca tct act tcg tat gac tat tgc      52
                              Met Ala Ser Thr Ser Tyr Asp Tyr Cys
                               1               5


aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg     100
Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
 10               15               20               25


ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg     148
Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
              30               35               40


att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt     196
Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu
              45               50               55


cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag     244
Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu
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            60                    65                    70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc    292
Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
        75                    80                    85


acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag    340
Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
    90                    95                    100                   105


aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act    388
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
                    110                   115                   120


aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg    436
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
                125                   130                   135


aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac    484
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
            140                   145                   150


tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg    532
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
        155                   160                   165


att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
170                   175                   180
```

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acatcttgga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag 645

ttctgagcgg gtcatggggc aacacggtta gcggggagag cacggggtag ccggagaagg 705

gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 765

ttgacccagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc 825

tcccaccctg agattgggca tggggtgcgg tgtggggggc atgtgctgcc tgttgttatg 885

ggtttttttt gcggggggggg ttgcttttttt ctggggtctt tgagctccaa aaaataaaca 945

cttcctttga gggagagcac acctt   970

<210> 93

<211> 331

<212> PRT

<213> Homo sapiens

<400> 93

Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe
1   5   10   15

Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn
                20   25   30

Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu

                35   40   45

Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala
         50   55   60

Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp
65   70   75   80

Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile
                      85   90   95

Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly
                  100   105   110

Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly
              115   120   125

Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr
         130   135   140

Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala
145   150   155   160

Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser
                  165   170   175

Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu
                  180   185   190

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Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser
        195   200   205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile
        210   215   220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr
225   230   235   240

Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala
                245   250   255

Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr
                260   265   270

Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu
                275   280   285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu
        290   295   300

Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln
305   310   315   320

Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His
                325   330

<210> 94

<211> 2039

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(1167)

<400> 94

attatgcaga tgcacggctg gaggtgggat ccacacagct cagaacagct ggatcttgct 60

cacactcttt caagagaagc ttccttgggt taagaaaaaa aacgaaccct tccagtcagg 120

tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg   177

                                                               Met
                                                                1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg   225
Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg
                5   10   15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa   273
Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu
            20   25   30

gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca   321
Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala
        35   40   45

gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att   369
Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile
50   55   60   65

gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt   417
Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe
                70   75   80

ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa   465
Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu
                85   90   95

aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc   513
Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys
        100   105   110

acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc   561
Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile
        115   120   125

atg tcc ctt gct ggt ctt gtt ttg gca cca ttt aca gca ggg acg agt   609
Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser
130   135   140   145

ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg   657
Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val
        150   155   160

act ggg atc acc acc agc atc gtg gag cac tca tac aca tca tca gca   705
                                323/735

Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala
          165   170   175

gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag   753
Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys
          180   185   190

gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt   801
Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu
          195   200   205

ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt   849
Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg
210   215   220   225

gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg   897
Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp
          230   235   240

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc   945
Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly
          245   250   255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act   993
Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr
          260   265   270

tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca   1041
Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser

```
                275              280              285

aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg    1089
Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg
290              295              300              305


cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc    1137
Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile
                310              315              320


tat cag cgt ctg aat cca tgc cat acc cac tgaccccaga ccagtgcagc      1187
Tyr Gln Arg Leu Asn Pro Cys His Thr His
                325              330


cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcatttt attagggggga 1247

taaagagggc aaggtaaagt ttatggagct gagtgttagt gactttggca tttctgtagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat 1367

gctggagcct ggaataaggg aggagagggg actggagagt gtggggaata ggaagaagaa 1427

atttccttta gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc 1487

agcaatgaga aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac 1547

ttttggatac agcagaagaa acagcggctc cactaccgac ctgcccccgg ttcgatgtcc 1607

ttccaagaat gaagtctttc cctggtgatg gtcccctgcc ctgtctttcc agcatccact 1667
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ctgtcttgtc ctcctggaag tgtatctcag tcagccagtg gcttcttgat gatggcggtg 1727

gaggtggtgg ttgtagtgtg atggatcccc tttaggttat ttaggggtat atgtcccctg 1787

cttgaaccct gaaggccagg taatgagcca tggccattgt ccccagctga ggaccaggtg 1847

tctctaaaaa cccaaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907

ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967

gggaggccgg atctctagag ccatcctgct gagtgccctg tgtgtaagtc ctaataaact 2027

cacctactca cc   2039

<210> 95

<211> 407

<212> PRT

<213> Homo sapiens

<400> 95

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
1   5   10   15

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
            20   25   30

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

```
              35                    40                    45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
         50                    55                    60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
 65                    70                    75                    80

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
                   85                    90                    95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
              100                   105                   110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
         115                   120                   125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
    130                   135                   140

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145                   150                   155                   160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
              165                   170                   175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
              180                   185                   190
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Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
        195   200   205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
        210   215   220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
        225   230   235   240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
            245   250   255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
            260   265   270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
            275   280   285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
        290   295   300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305   310   315   320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
            325   330   335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
            340   345   350

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Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
       355   360   365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
       370   375   380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
385   390   395   400

Val Cys Lys Tyr Lys Leu Leu
                 405

<210> 96

<211> 1409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (181)..(1401)

<400> 96

gctgtgcttg gcgcgtaccg tgcggtccct gtagttggag acgggcggt cgcgcggcct 60

ttcccactag ccggagtagc ctctagttcg ttagtcaaaa cgtgaaaaaa aaagacctgc 120

tttgccctgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

```
atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg      228
Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
 1               5                  10                  15


ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa      276
Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
                20                  25                  30


tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga      324
Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
                35                  40                  45


cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act      372
Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
    50                  55                  60


gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa      420
Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
65                  70                  75                  80


aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga      468
Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
                85                  90                  95


cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg      516
His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
                100                 105                 110
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att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc   564
Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
          115   120   125

tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc   612
Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
      130   135   140

ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc   660
Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145   150   155   160

ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act   708
Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
              165   170   175

aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca   756
Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
          180   185   190

ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa   804
Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
          195   200   205

ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc   852
Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
      210   215   220

atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa   900

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225   230   235   240

gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga   948
Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
          245   250   255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg   996
Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
          260   265   270

cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac   1044
Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
          275   280   285

ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc   1092
Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
          290   295   300

aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta   1140
Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305   310   315   320

atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta   1188
Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
          325   330   335

gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca   1236
Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
                332/735

340   345   350

aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca   1284
Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
        355   360   365

gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa   1332
Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
        370   375   380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt   1380
Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
385   390   395   400

gtg tgc aaa tat aaa cta tta taaaatcg   1409
Val Cys Lys Tyr Lys Leu Leu
        405

<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
1   5   10   15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

                20   25   30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
            35   40   45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
         50   55   60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
    65   70   75   80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
                  85   90   95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
                  100   105   110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
            115   120   125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val
         130   135   140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
145   150   155   160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
                  165   170   175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
    180   185   190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
    195   200   205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
    210   215   220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225   230   235   240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
    245   250   255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
    260   265   270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
    275   280   285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
    290   295   300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305   310   315   320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
    325   330   335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
        340   345   350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
        355   360   365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
        370   375   380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385   390   395   400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
            405   410   415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
        420   425   430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
        435   440   445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
        450   455   460

Asp
465

<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477)..(1871)

<400> 98

gttaacttcc tgacccagga agtggcagca acagagggga ctagcagcga atatacttta   60

caccaaatct cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag   120

ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagaggggcc   180

tggtgtatca ctggaggaaa tagcctgcca aggaatacac gtcttcagaa gaagttctgt   240

gtggcttcaa gagactgatc aaattgtgag aggaaaacag cctacccggt cctctttct   300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag   360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat   420

tctggctgct tcatctccat ctctagagcc aatattggag cttttcaata aaagct atg   479

                                                                   Met

                                                                    1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc   527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
          5   10   15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac   575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
       20   25   30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa   623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
       35   40   45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca   671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
50   55   60   65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att   719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
         70   75   80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga   767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
       85   90   95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg   815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
      100   105   110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt   863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
                338/735

             115   120   125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca   911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr
130   135   140   145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca   959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr
                    150   155   160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa   1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln
                         165   170   175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa   1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
                         180   185   190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg   1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
                    195   200   205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa   1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
210   215   220   225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc   1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
                         230   235   240

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cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct    1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
        245              250              255


gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg    1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
        260              265              270


tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt    1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
        275              280              285


cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta    1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
290              295              300              305


att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag    1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
        310              315              320


aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg    1487
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu
        325              330              335


ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt    1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
        340              345              350
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ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag    1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
    355             360             365


agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc    1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
370             375             380             385


agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act    1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
            390             395             400


tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac    1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
                405             410             415


tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac    1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
        420             425             430


atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat    1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
    435             440             445


ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac    1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
450             455             460             465


taaggaaaag agcagaagct ccttggttta accagcacag agaaataat ataaatccca 1931
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taagggcag   1940

<210> 99

<211> 465

<212> PRT

<213> Homo sapiens

<400> 99

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
1   5   10   15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
                20   25   30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
            35   40   45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
        50   55   60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
65   70   75   80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
                85   90   95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys

                100   105   110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
        115   120   125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val
        130   135   140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
145   150   155   160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
                165   170   175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
                180   185   190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
            195   200   205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
        210   215   220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225   230   235   240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
                245   250   255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
        260   265   270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
        275   280   285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
        290   295   300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305   310   315   320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
                325   330   335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
        340   345   350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
        355   360   365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
        370   375   380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385   390   395   400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
                405   410   415

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Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
       420   425   430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
       435   440   445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
       450   455   460

Asp

465

<210> 100

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477)..(1871)

<400> 100

gttaacttcc tgacccagga agtggcagca acagagggga ctagcagcga atatacttta 60

caccaaatct cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120

ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcca aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgatc aaattgtgag aggaaaacag cctacccggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcatctccat ctctagagcc aatattggag cttttcaata aaagct atg 479

                                                                Met

                                                                  1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc   527
Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
              5   10   15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac   575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
                 20   25   30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa   623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
          35   40   45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca   671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
 50   55   60   65

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ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att    719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
                70                  75                  80


gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga    767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
            85                  90                  95


gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg    815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
        100                 105                 110


cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt    863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
        115                 120                 125


gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca    911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr
130                 135                 140                 145


aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca    959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr
                150                 155                 160


gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa    1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln
            165                 170                 175


aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa    1055
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●

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Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
        180                 185                 190


gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg     1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
        195                 200                 205


agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa     1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
210                 215                 220                 225


ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc     1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
                230                 235                 240


cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct     1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
                245                 250                 255


gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg     1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
        260                 265                 270


tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt     1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
        275                 280                 285


cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta     1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
                        348/735
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290   295   300   305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag   1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
                    310   315   320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg   1487
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu
                    325   330   335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt   1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
                    340   345   350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag   1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
                    355   360   365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc   1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
370   375   380   385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act   1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
                    390   395   400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac   1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
                    405   410   415
                         349/735

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tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac    1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
        420                 425                 430


atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat    1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
        435                 440                 445


ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac    1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
450                 455                 460                 465


taaggaaaag agcagaagct ccttggttta accagcacag agaaataat ataaatccca 1931


taagggcag                                                          1940
```

<210> 101

<211> 685

<212> PRT

<213> Homo sapiens

<400> 101

```
Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
1               5                   10                  15


Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
            20                  25                  30
```

```
Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
         35                  40                  45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
         50                  55                  60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
65                  70                  75                  80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
                 85                  90                  95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
                 100                 105                 110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
                 115                 120                 125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
         130                 135                 140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
145                 150                 155                 160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
                 165                 170                 175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
                         351/735
```

                180   185   190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
        195   200   205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
        210   215   220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
225   230   235   240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
                245   250   255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr
                260   265   270

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
        275   280   285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
        290   295   300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
305   310   315   320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln
                325   330   335

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
      340   345   350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
      355   360   365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr
      370   375   380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
385   390   395   400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr
              405   410   415

Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr
              420   425   430

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
      435   440   445

Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
      450   455   460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
465   470   475   480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
              485   490   495

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
        500   505   510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
        515   520   525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val
        530   535   540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
545   550   555   560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
                565   570   575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
        580   585   590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
        595   600   605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
        610   615   620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625   630   635   640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
                          354/735

```
                    645                 650                 655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
             660                 665                 670


Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
             675                 680                 685
```

<210> 102

<211> 2783

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (128)..(2182)

<400> 102

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gcacaagtgg accggggtgt tgggtgctag tcggcaccag aggcaagggt gcgaggacca 60


cggccggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtgc ggggcggcaa 120


ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc      169
        Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser
         1               5                   10


acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg      217
Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser
```

```
              15                      20                      25                      30

aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag    265
Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln
                        35                      40                      45


tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat    313
Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His
                        50                      55                      60


tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act    361
Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr
              65                      70                      75


ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca    409
Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala
              80                      85                      90


aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca    457
Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala
95                      100                     105                     110


aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag    505
Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys
                        115                     120                     125


att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta    553
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val
              130                     135                     140
```

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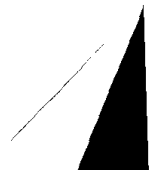
```
gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc    601
Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu
        145                 150                 155


ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga    649
Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg
        160                 165                 170


aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg    697
Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val
175                 180                 185                 190


tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc    745
Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu
                195                 200                 205


aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg    793
Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly
        210                 215                 220


gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga    841
Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg
        225                 230                 235


acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa    889
Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys
        240                 245                 250
```

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```
caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg     937
Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met
255             260             265             270


tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa     985
Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys
            275             280             285


gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca    1033
Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser
            290             295             300


ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac    1081
Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn
        305             310             315


cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt    1129
Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe
    320             325             330


ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca    1177
Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr
335             340             345             350


gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa    1225
Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys
            355             360             365


gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att    1273
```
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Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile
370   375   380

gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt   1321
Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu
385   390   395

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac   1369
Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His
400   405   410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct   1417
Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser
415   420   425   430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg   1465
Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg
435   440   445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc   1513
Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys
450   455   460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt   1561
Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val
465   470   475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa   1609
Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys
359/735

480   485   490

gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac   1657
Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr
495   500   505   510

tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt   1705
Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly
                 515   520   525

gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa   1753
Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys
                 530   535   540

aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca   1801
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala
                 545   550   555

aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac   1849
Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr
        560   565   570

ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct   1897
Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro
575   580   585   590

agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta   1945
Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu
                 595   600   605

```
aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag    1993
Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln
        610                 615                 620


gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat    2041
Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn
        625                 630                 635


gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act    2089
Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr
        640                 645                 650


ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa    2137
Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys
655                 660                 665                 670


aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac        2182
Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
                675                 680                 685


tgaaagactt ttcgaatgga ccctatggga ctcctctttt ccactgtgag atctacaggg 2242


aacccaaaag aatgatctag agtatgttga agaagatgga catgtggtgg tacgaaaaca 2302


attcccctgt ggcctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362


actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttaaaa 2422
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ggttttttcag acaattttgc agaaaggtgc attgattctt aaattctctc tgttgagagc 2482

atttcagcca gaggactttg gaactgtgaa tatacttcct gaaggggagg gagaagggag 2542

gaagctccca tgttgtttaa aggctgtaat tggagcagct tttggctgcg taactgtgaa 2602

ctatggccat atataatttt ttttcattaa tttttgaaga tacttgtggc tggaaaagtg 2662

cattccttgt taataaactt tttatttatt acagcccaaa gagcagtatt tattatcaaa 2722

atgtcttttt ttttatgttg accattttaa accgttggca ataaagagta tgaaaacgca 2782

g   2783

<210> 103

<211> 161

<212> PRT

<213> Homo sapiens

<400> 103

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
1   5   10   15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
            20   25   30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
        35   40   45

```
Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
        50              55              60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
    65              70              75              80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys
                85              90              95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
                100             105             110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
            115             120             125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
        130             135             140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145             150             155             160

Leu
```

<210> 104

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 104

cctttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111
           Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
           1   5   10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac   159
Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
15   20   25   30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg   207
Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
            35   40   45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat   255
Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
            50   55   60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg   303
Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
            65   70   75

```
gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg     351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met
        80                  85                  90


tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac     399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
 95              100                 105                 110


gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg     447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
                115                 120                 125


tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag     495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
                130                 135                 140


gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac     543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
        145                 150                 155


aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg            592
Lys Arg Leu
        160


aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tggtggtctc 652


acctctccag ggggcccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712


aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772
```

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt cttaattttt 1132

tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcccc tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct tttggtctga aatactttcg aacagaattt cttttttta 1372

aaaaaaaaca gagatggggt cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589

<210> 105

<211> 161

<212> PRT

<213> Homo sapiens

<400> 105

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
1   5   10   15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
                20   25   30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
                35   40   45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
        50   55   60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
65   70   75   80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys
                    85   90   95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
                100   105   110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
                            367/735

```
            115                 120                 125


Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
        130                 135                 140


Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145                 150                 155                 160


Leu
```

<210> 106

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 106

ccttttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60


```
ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc  111
          Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
           1               5                   10
```

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac   159

```
Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
15                  20                  25                  30
```

```
agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg     207
Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
                35                  40                  45
```

```
ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat     255
Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
                50                  55                  60
```

```
acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg     303
Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
                65                  70                  75
```

```
gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg     351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met
                80                  85                  90
```

```
tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac     399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
95                  100                 105                 110
```

```
gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg     447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
                115                 120                 125
```

```
tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag     495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
```

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```
           130              135              140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac   543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
           145              150              155


aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg         592
Lys Arg Leu
     160


aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tggtggtctc 652


acctctccag ggggcccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712


aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772


cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832


ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctctttttc 892


ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952


ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012


ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072


tgagattctg taactgcaga cttcattagc acacagattc actttaattt cttaattttt 1132


tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192
```

atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcccc tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct tttggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaca gagatggggt cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt   1589

<210> 107

<211> 249

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val
1   5   10   15

Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val
                20   25   30

Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys
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```
        35                    40                    45

Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn
        50                    55                    60

Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu
        65                    70                    75                    80

Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met
                      85                    90                    95

Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val
                     100                   105                   110

Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys
             115                   120                   125

Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro
        130                   135                   140

Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro
145                   150                   155                   160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met
                     165                   170                   175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu
             180                   185                   190
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Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His
      195   200   205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val
      210   215   220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile
225   230   235   240

Gly Phe Phe Leu Gly Lys Phe Ile Leu
            245

<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)..(978)

<400> 108

agtgcgcgtg gccgtggcgg ctggtgtggg gttgagtcag ttgtgggacc cggagctgct 60

gacccagcgg gtggcccacc gaaccggtga cacagcggca ggcgttaggg ctcgggagcc 120

gcgagcctgg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgccccc 180

agtcagcaaa ccgccgccgc gggcgcgccc ccgctctgcg ctgtctctcc g atg gcg   237

                                                                   Met Ala

                                                                1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat   285

Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp

             5   10   15

ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act   333

Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr

          20   25   30

aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa   381

Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys

          35   40   45   50

gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga   429

Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly

                  55   60   65

att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc   477

Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro

                  70   75   80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag   525

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln

          85   90   95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa   573

```
Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys
    100             105             110


gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt    621
Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe
115             120             125             130


gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa    669
Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys
            135             140             145


gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca    717
Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro
            150             155             160


cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag    765
His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu
            165             170             175


tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg    813
Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg
    180             185             190


cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat    861
His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp
195             200             205             210


aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt    909
Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser
```

215   220   225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc   957
Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe
            230   235   240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttctt   1008
Phe Leu Gly Lys Phe Ile Leu
            245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcat tggtagtatg 1068

gcccacggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacggtta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtcc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308

tgttatttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368

atttagattg ctaatcccac tcattcagga aatgccaaga ggtattcctt ggggaaatgg 1428

tgcctcttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tgttgactga gtttttcatc cttacaatcc tgtcccatgg 1548

tatttaacat aaaaaaaaat aaaactgtta acagattctt gctcgat   1595

<210> 109

<211> 540

<212> PRT

<213> Homo sapiens

<400> 109

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
1   5   10   15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
                20   25   30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
            35   40   45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
        50   55   60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
65   70   75   80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
                85 ·   90   95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
                100   105   110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
         115   120   125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
         130   135   140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145   150   155   160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
                   165   170   175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
                   180   185   190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
              195   200   205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210   215   220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225   230   235   240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
                   245   250   255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
                   260   265   270

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Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
        275   280   285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
        290   295   300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305   310   315   320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
        325   330   335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
        340   345   350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
        355   360   365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
        370   375   380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385   390   395   400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg
                405   410   415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
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                420                      425                      430

    Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
            435                  440                  445

    Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
            450                  455                  460

    Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
    465                  470                  475                  480

    Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
                    485                  490                  495

    Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
            500                  505                  510

    Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
            515                  520                  525

    Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
        530                  535                  540
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<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 110

aaccgtaaca gccaccagac aagcttcagt ggccggccct tcacatccag acttgcctga 60

gaggacccac ctctgagtgt ccagtggtca gttgccccag g atg ggg acc aca gcc 116

                                           Met Gly Thr Thr Ala

                                           1   5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct   164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

            10   15   20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac   212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

                25   30   35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga   260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

            40   45   50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt   308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

            55   60   65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct   356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

| | 70 | | | 75 | | | | 80 | | | | 85 | | | |

```
ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa    404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
                 90              95              100
```

```
gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg    452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
                 105             110             115
```

```
ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca    500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
                 120             125             130
```

```
ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag    548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
                 135             140             145
```

```
cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat    596
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp
150             155             160             165
```

```
ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc    644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys
                 170             175             180
```

```
ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag    692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln
                 185             190             195
```

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg   740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
         200   205   210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc   788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
         215   220   225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt   836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
230   235   240   245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg   884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
            250   255   260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca   932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro
            265   270   275

cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg   980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser
         280   285   290

ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc   1028
Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
         295   300   305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg   1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
310   315   320   325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg   1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
          330   335   340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt   1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
          345   350   355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag   1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
       360   365   370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc   1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser
    375   380   385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat   1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr
390   395   400   405

gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc   1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu
          410   415   420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat   1412

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Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His
          425   430   435

                            .

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca   1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro
          440   445   450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc   1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile
          455   460   465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc   1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu
470   475   480   485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc   1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile
             490   495   500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc   1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala
          505   510   515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc   1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser
          520   525   530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga   1751
Thr Ser Glu Pro Lys Glu Glu
                       385/735

535   540

tgggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg   1810

<210> 111

<211> 540

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
1   5   10   15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
            20   25   30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
        35   40   45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
        50   55   60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
65   70   75   80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
                85   90   95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
                100   105   110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
                115   120   125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
                130   135   140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145   150   155   160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
                165   170   175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
                180   185   190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
                195   200   205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
                210   215   220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225   230   235   240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
                245   250   255

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Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
          260   265   270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
          275   280   285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
          290   295   300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305   310   315   320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
          325   330   335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
          340   345   350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
          355   360   365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
     370   375   380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385   390   395   400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
                              388/735

```
                405                    410                    415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
            420                    425                    430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
            435                    440                    445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
            450                    455                    460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465                    470                    475                    480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
                485                    490                    495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
                500                    505                    510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
                515                    520                    525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
                530                    535                    540
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<210> 112

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 112

aaccgtaaca gccaccagac aagcttcagt ggccggccct tcacatccag acttgcctga 60

gaggacccac ctctgagtgt ccagtggtca gttgccccag g atg ggg acc aca gcc 116

                                         Met Gly Thr Thr Ala

                                        1   5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct   164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

          10   15   20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac   212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

          25   30   35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga   260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

          40   45   50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt   308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

          55   60   65

```
gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct    356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
70              75              80              85


ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa    404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
                90              95              100


gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg    452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
                105             110             115


ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca    500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
            120             125             130


ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag    548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
            135             140             145


cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat    596
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp
150             155             160             165


ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc    644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys
            170             175             180
```

```
ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag     692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln
            185                 190                 195


tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg     740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
            200                 205                 210


gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc     788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
        215                 220                 225


cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt     836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
230                 235                 240                 245


gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg     884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
            250                 255                 260


cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca     932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro
            265                 270                 275


cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg     980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser
            280                 285                 290


ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc     1028
```

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Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
      295   300   305

aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg   1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
310   315   320   325

cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg   1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
              330   335   340

gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt   1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
              345   350   355

aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag   1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
      360   365   370

tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc   1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser
      375   380   385

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat   1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr
390   395   400   405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc   1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu
                         393/735

```
                410                    415                    420


     atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat    1412
     Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His
             425                    430                    435



     att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca    1460
     Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro
             440                    445                    450



     ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc    1508
     Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile
             455                    460                    465



     aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc    1556
     Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu
     470                    475                    480                    485



     tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc    1604
     Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile
                    490                    495                    500



     aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc    1652
     Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala
             505                    510                    515



     aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc    1700
     Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser
             520                    525                    530
```

```
acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga        1751
Thr Ser Glu Pro Lys Glu Glu
    535                 540
```

```
tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg   1810
```

<210> 113

<211> 382

<212> PRT

<213> Homo sapiens

<400> 113

```
Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala
 1               5                   10                  15
```

```
Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
                20                  25                  30
```

```
Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
            35                  40                  45
```

```
Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
        50                  55                  60
```

```
Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65                  70                  75                  80
```

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
              85   90   95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
                 100   105   110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
                 115   120   125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
             130   135   140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145   150   155   160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
                 165   170   175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
                 180   185   190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
                 195   200   205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
    210   215   220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225   230   235   240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
          245   250   255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
          260   265   270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
          275   280   285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
          290   295   300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305   310   315   320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
          325   330   335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
          340   345   350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
          355   360   365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
370   375   380

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<210> 114

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

<400> 114

aactttacg aggtatcagc actttctttt cattaggggg aaggcgtgag gaaagtacca 60

aacagcagcg gagttttaaa ctttaaatag acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233
                          Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
                           1   5   10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca   281
Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
             15   20   25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca   329
Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser
             30   35   40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct   377

```
                Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
                     45                  50                  55


      ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg        425
      Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
       60                  65                  70                  75


      cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg        473
      Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
                       80                  85                  90


      tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac        521
      Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
                       95                  100                 105


      aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg        569
      Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
                  110                 115                 120


      gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att        617
      Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
           125                 130                 135


      gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac        665
      Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
      140                 145                 150                 155


      atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg        713
      Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu
```

                    160   165   170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc   761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys
              175   180   185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc   809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro
              190   195   200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg   857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val
         205   210   215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc   905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly
220   225   230   235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt   953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser
              240   245   250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat   1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr
              255   260   265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct   1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
              270   275   280

```
cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc      1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
    285             290             295


aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca      1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala
300             305             310             315


gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat      1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
                320             325             330


gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta      1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
            335             340             345


gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct      1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
    350             355             360


tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac      1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
    365             370             375


ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt             1386
Leu Glu Ile
380
```

ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgatc cggtggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggta 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046

ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt tttttgagc taaagtcagg gaatcaagcc atgcttaata tttaacaatc 2166

acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

tataaactca caaacacaga tttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286

```
tctcatggat ttttgtggtg tgggccaata tggtgtttac attatataat tcctgctgtg 2346

gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406

atactggttt tgttaattat gattctttat tttctctcct tttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttccttttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaattttagt actgtaaaca ggctttagtc attaatgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaaatgt gcctaaatga attttgcagt aactggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtctttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttatttt ggaatgcaag agaggttgaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcat gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttgtt tgacattcca tgttaaacta cggtcatgtt cagcttcatt gcatgtaatg 3006

tagacctagt ccatcagatc atgtgttctg gagagtgttc tttattcaat aaagtttttaa 3066

tttagtat                                                    3074
```

<210> 115

<211> 382

<212> PRT

<213> Homo sapiens

<400> 115

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala
1   5   10   15

Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
                20   25   30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
            35   40   45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
        50   55   60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65   70   75   80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
                85   90   95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
                100   105   110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys

```
           115              120                 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
     130              135                 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145              150                 155                 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
                 165              170                 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
                 180              185                 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
                 195              200                 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
     210              215                 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225              230                 235                 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
                 245              250                 255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
                 260              265                 270
```

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Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
                275   280   285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
                290   295   300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305   310   315   320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
                325   330   335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
                340   345   350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
                355   360   365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
                370   375   380

<210> 116

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

<400> 116

aacttttacg aggtatcagc actttctttt cattagggggg aaggcgtgag gaaagtacca 60

aacagcagcg gagttttaaa ctttaaatag acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233
                    Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
                     1   5   10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281
Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
        15   20   25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329
Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser
        30   35   40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377
Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
        45   50   55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
60   65   70   75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg   473
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
               80   85   90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac   521
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
               95   100   105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg   569
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
             110   115   120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att   617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
        125   130   135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac   665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
140   145   150   155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg   713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu
             160   165   170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc   761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys
        175   180   185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc   809

```
                    Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro
                        190             195             200


acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg        857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val
    205             210             215


tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc        905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly
220             225             230             235


gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt        953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser
                240             245             250


ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat       1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr
            255             260             265


ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct       1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
            270             275             280


cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc       1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
285             290             295


aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca       1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala
```

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```
       300                    305                    310                    315
```

```
gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat   1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
                        320                    325                    330
```

```
gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta   1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
                335                    340                    345
```

```
gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct   1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
                350                    355                    360
```

```
tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac   1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
                365                    370                    375
```

```
ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt          1386
Leu Glu Ile
380
```

```
ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgatc cggtggaggt 1446
```

```
ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506
```

```
tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566
```

```
gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626
```

catagataaag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggta 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc acttttttcat cattcctcag 2046

ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcttaata tttaacaatc 2166

acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

tataaactca caaacacaga tttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286

tctcatggat ttttgtggtg tgggccaata tggtgtttac attatataat tcctgctgtg 2346

gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406

atactggttt tgttaattat gattctttat tttctctcct tttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaattttagt actgtaaaca ggctttagtc attaatgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaaatgt gcctaaatga attttgcagt aactggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttattt ggaatgcaag agaggttgaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcat gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttgtt tgacattcca tgttaaacta cggtcatgtt cagcttcatt gcatgtaatg 3006

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tttagtat   3074

<210> 117

<211> 398

<212> PRT

<213> Homo sapiens

<400> 117

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Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
1               5                   10                  15

Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala
            20                  25                  30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
            35                  40                  45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
    50                  55                  60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65                  70                  75                  80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
                85                  90                  95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
                100                 105                 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
                115                 120                 125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
    130                 135                 140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145                 150                 155                 160
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Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
            165   170   175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
            180   185   190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
            195   200   205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
    210   215   220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225   230   235   240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
                245   250   255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
            260   265   270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
            275   280   285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
    290   295   300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
                            414/735

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
            325   330   335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
            340   345   350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
            355   360   365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
    370   375   380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
385   390   395

<210> 118

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 118

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aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc   111
              Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
              1   5   10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag   159
Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu
          15   20   25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act   207
Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
          30   35   40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg   255
Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
          45   50   55   60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag   303
Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
              65   70   75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag   351
Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
          80   85   90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca   399
Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
          95   100   105

```
gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg    447
Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
    110             115             120


aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt    495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
125             130             135             140


ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga    543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
            145             150             155


agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc    591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
            160             165             170


acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc    639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
        175             180             185


ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc    687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
    190             195             200


ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg    735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
205             210             215             220


acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca    783
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Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
                    225   230   235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag   831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
                240   245   250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta   879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
                255   260   265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt   927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
            270   275   280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca   975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
285   290   295   300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa   1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu
                    305   310   315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga   1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
                320   325   330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat   1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
                        418/735

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            335                    340                    345


gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag    1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys
    350                    355                    360


tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag    1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu
365                    370                    375                    380


aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa    1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln
                385                    390                    395


gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca    1319
Glu Leu


ggacaaaatg caaacttttt tttttctga gacagagtct tgctctgtcg ccaagttgca  1379


gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa  1439


aaaaaaaaaa aaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc  1499


aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt  1559


tggatacagg agaagaaaca gcggctccac tacagaccca gccccaggtt caatgtcctc  1619


cgaagaatga agtctttccc tggtgatggt cccctgccct gtctttccag catccactct  1679
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cccttgtcct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttacccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatc   2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
1   5   10   15

Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala
                20   25   30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
        35   40   45

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Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
        50   55   60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65   70   75   80

Thr Gln Asn Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
                85   90   95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
            100   105   110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
            115   120   125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
        130   135   140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145   150   155   160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
                165   170   175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
                180   185   190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
                        421/735

                195   200   205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
        210   215   220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225   230   235   240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
                245   250   255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
                260   265   270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
                275   280   285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
        290   295   300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
305   310   315   320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
                325   330   335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
                340   345   350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
      355   360   365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
      370   375   380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
385   390   395

<210> 120

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 120

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aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc   111
                 Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
                 1   5   10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag   159
Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu
         15   20   25

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gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act    207
Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
     30                  35                  40


gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg    255
Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
 45                  50                  55                  60


gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag    303
Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
                 65                  70                  75


gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag    351
Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
             80                  85                  90


gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca    399
Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
             95                 100                 105


gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg    447
Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
        110                 115                 120


aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt    495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
125                 130                 135                 140
```

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ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga   543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
                145                 150                 155


agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc   591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
                160                 165                 170


acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc   639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
                175                 180                 185


ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc   687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
            190                 195                 200


ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg   735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
205                 210                 215                 220


acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca   783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
                225                 230                 235


caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag   831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
                240                 245                 250


gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta   879
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Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
       255   260   265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt   927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
       270   275   280

gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca   975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
285   290   295   300

gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa   1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu
             305   310   315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga   1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
       320   325   330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat   1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
       335   340   345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag   1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys
       350   355   360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag   1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

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        365                 370                 375                 380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa     1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln
                    385                 390                 395


gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca     1319
Glu Leu


ggacaaaatg caaacttttt tttttctga gacagagtct tgctctgtcg ccaagttgca   1379


gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa  1439


aaaaaaaaa aaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc   1499


aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt  1559


tggatacagg agaagaaaca gcggctccac tacagaccca gccccaggtt caatgtcctc  1619


cgaagaatga agtctttccc tggtgatggt cccctgccct gtctttccag catccactct  1679


cccttgtcct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg  1739


ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga  1799


acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct  1859


gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct  1919
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cttacccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatc   2054

<210> 121

<211> 108

<212> PRT

<213> Homo sapiens

<400> 121

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe
1   5   10   15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu
            20   25   30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys
            35   40   45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
        50   55   60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65   70   75   80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala

     85   90   95

  Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
       100   105

<210> 122

<211> 1546

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)..(412)

<400> 122

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gcccgcccgc tcagcgtccg ccgccgcc atg gga gtg cag gtg gaa acc atc   112
               Met Gly Val Gln Val Glu Thr Ile
                1   5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg   160
Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val
  10   15   20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc   208
Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser
 25   30   35   40

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg   256
Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val
            45   50   55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga   304
Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg
            60   65   70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac   352
Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His
            75   80   85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt   400
Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
            90   95   100

cta aaa ctg gaa tgacaggaat ggcctcctcc cttagctccc tgttcttgga   452
Leu Lys Leu Glu
105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgctt ccgacacctc tgtttcctct tcccctttct cctcgtatgt gtgtttacct 632

aaactatatg ccataaacct caagttactc attttatttt gttttcattt tgggggtgaag 692

attcagtttc agtcttttgg atataggttt ccaattaagt acatggtcaa gtattaacag 752

cacaagtggt aggttaacat tagaatagga attggtgttg ggggggggt ttgcaagaat 812

attttatttt aatttttgg atgaaatttt tatctattat atattaaaca ttcttgctgc 872

tgcgctgcaa agccatagca gatttgaggc gctgttgagg actgaattac tctccaagtt 932

gagagatgtc tttgggttaa attaaaagcc ctacctaaaa ctgaggtggg gatggggaga 992

gcctttgcct ccaccattcc cacccaccct ccccttaaac cctctgcctt tgaaagtaga 1052

tcatgttcac tgcaatgctg gacactacag gtatctgtcc ctgggccagc agggacctct 1112

gaagccttct ttgtggcctt tttttttttt tcatcctgtg gtttttctaa tggactttca 1172

ggaattttgt aatctcataa ctttccaagc tccaccactt cctaaatctt aagaacttta 1232

attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtgaa agcccagcca 1292

tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggtcatcgc agcttcagca 1352

tctcctgttt tttgatgctt ggctccctct gctgatctca gtttcctggc ttttcctccc 1412

tcagcccctt ctcacccctt tgctgtcctg tgtagtgatt tggtgagaaa tcgttgctgc 1472

acccttcccc cagcaccatt tatgagtctc aagtttatt attgcaataa aagtgcttta 1532

tgccggcttt tctc   1546

<210> 123

<211> 679

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly

1   5   10   15

Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala

                20   25   30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe

            35   40   45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile

        50   55   60

Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys

65   70   75   80

Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn

                85   90   95

Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly

                100   105   110

Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser
          115   120   125

Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala
          130   135   140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met
145   150   155   160

Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu
                    165   170   175

Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro
                    180   185   190

Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile
                    195   200   205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
          210   215   220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val
225   230   235   240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
                    245   250   255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
                    260   265   270

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Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser
        275   280   285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala
        290   295   300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys
305   310   315   320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val
                325   330   335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val
                340   345   350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn
                355   360   365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp
        370   375   380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val
385   390   395   400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn
                405   410   415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser
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                420   425   430

Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu
        435   440   445

Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr
        450   455   460

Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile
465   470   475   480

Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser
                485   490   495

Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser
                500   505   510

Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe
        515   520   525

Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala
        530   535   540

Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr
545   550   555   560

Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu
                565   570   575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
            580   585   590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
            595   600   605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His
            610   615   620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
625   630   635   640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
            645   650   655

Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
            660   665   670

Arg Tyr Val Ile Leu Arg Met
            675

<210> 124

<211> 2916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(2117)

<400> 124

ttttgatac ctcatattct gtttacacat cttgaaaggc gctcagtagt tctcttacta 60

aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113

                Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala

                1   5   10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161

Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu

       15   20   25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209

Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp

       30   35   40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257

Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu

       45   50   55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305

Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val

60   65   70   75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353

Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp

       80   85   90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc   401
Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val
             95   100   105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg   449
Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu
            110   115   120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt   497
Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly
            125   130   135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg   545
Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu
140   145   150   155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att   593
Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile
            160   165   170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag   641
Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys
            175   180   185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc   689
Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala
            190   195   200

tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg   737
                   438/735

Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro
    205   210   215

ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg   785
Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser
220   225   230   235

gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt   833
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys
                      240   245   250

ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct   881
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser
                      255   260   265

gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa   929
Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu
                  270   275   280

gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct   977
Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser
    285   290   295

gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga   1025
Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg
300   305   310   315

aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag   1073
Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu
                      439/735

                    320   325   330

agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc   1121
Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr
               335   340   345

gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt   1169
Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser
               350   355   360

caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac   1217
Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His
          365   370   375

acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta   1265
Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu
380   385   390   395

cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc   1313
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro
               400   405   410

tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc   1361
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly
          415   420   425

atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa   1409
Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu
          430   435   440

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gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att    1457
Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile
    445             450             455


cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac    1505
Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His
460             465             470             475


tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt    1553
Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly
            480             485             490


gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat    1601
Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp
            495             500             505


aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc    1649
Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala
            510             515             520


tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att    1697
Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile
            525             530             535


ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct    1745
Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser
540             545             550             555
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tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt      1793
Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly
            560                 565                 570


atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg      1841
Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met
            575                 580                 585


ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa      1889
Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu
            590                 595                 600


ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc      1937
Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro
        605                 610                 615


atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg      1985
Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp
620                 625                 630                 635


ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt      2033
Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe
            640                 645                 650


atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc      2081
Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala
            655                 660                 665


atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt          2127
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Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met
     670   675

tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga 2187

atgattacag tgttaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg 2247

aagtgttact tgtgctataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgaggtcc cctttccttc tgggctgtga 2367

attcctgtac atatttctct acttttgta tcaggcttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc tttgaacaca gtgaaaattt aaattagtaa ctttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847

ttaaatggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907

agtttttag

2916

<210> 125

<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

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Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala
1               5                   10                  15


Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu
            20                  25                  30


Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys
        35                  40                  45


Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu
    50                  55                  60


Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro
65                  70                  75                  80


Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp
                85                  90                  95


Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln
            100                 105                 110
```

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Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
          115   120   125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
          130   135   140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145   150   155   160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
                    165   170   175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
                    180   185   190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu
                    195   200   205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
          210   215   220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
225   230   235   240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
                    245   250   255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
                              445/735

```
           260                 265                 270
```

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met

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           275                 280                 285
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<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(944)

<400> 126

tcaacgcctg cctcccctcg agcgtcctca gcgcagccgc cgcccgcgga gccagcacga 60

acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113
                      Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln
                       1   5   10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag   161
Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln
            15   20   25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc   209
Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr
        30   35   40

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cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg   257
Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val
     45   50   55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc   305
Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala
60   65   70   75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag   353
Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln
           80   85   90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac   401
Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr
           95   100   105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc   449
Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg
       110   115   120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt   497
Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly
       125   130   135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg   545
Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu
140   145   150   155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac   593
Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn
                160   165   170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac   641
Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn
                175   180   185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc   689
Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala
                190   195   200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag   737
Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu
        205   210   215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg   785
Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly
220   225   230   235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag   833
Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu
                240   245   250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt   881
Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu
                255   260   265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta   929
                        448/735

Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val
      270   275   280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt   984
Gly Leu Tyr Ala Met
    285

ccggtggaag gccttctttc tagagaggga attctcttgg ctggcttcct taccgtgggc   1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa   1104

ggagcctatg gcatcttccc caacgaaaag cacatccagg caatggccta aacttcagag   1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag   1224

acaccctaat gtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt   1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag   1344

atgttgtgtc ttgtgttttt gtcttatttt tgttggagcc actctgttcc tggctcagcc   1404

tcaaatgcag tatttttgtt gtgttctgtt gttttatag cagggttggg gtggtttttg   1464

agccatgcgt gggtggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg   1524

tgtgaaataa taaacaacat tgtctg   1550

<210> 127

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1   5   10   15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

            20   25   30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

            35   40   45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

        50   55   60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

65   70   75   80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

                85   90   95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

                100   105   110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys

                115   120   125

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Ile Lys Cys Val Ala Phe Asp
    130              135
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<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(454)

<400> 128

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cttctgacag ctggtgcgcc tgcccgggaa catcctcctg gactcaatc atg gct tgt    58
                                                         Met Ala Cys
                                                          1


ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga    106
Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg
         5               10              15


gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg    154
Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu
 20              25              30              35


ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac    202
Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn
             40              45              50
```

```
gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg     250
Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
            55                  60                  65


gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga     298
Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
            70                  75                  80


agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc     346
Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
            85                  90                  95


aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg     394
Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
100                 105                 110                 115


gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt     442
Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys
                120                 125                 130


gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc         494
Val Ala Phe Asp
                135


ctctgctccc ctg                                                      507
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<210> 129

<211> 662

<212> PRT

<213> Homo sapiens

<400> 129

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn

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            20   25   30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp

            35   40   45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys

        50   55   60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser

65   70   75   80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr

                85   90   95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu

                100   105   110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys

            115   120   125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
   130   135   140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
145   150   155   160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro
           165   170   175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
           180   185   190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
           195   200   205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
   210   215   220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
225   230   235   240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu
           245   250   255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr
           260   265   270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln
       275   280   285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys
    290   295   300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val
305   310   315   320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala
            325   330   335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe
            340   345   350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp
            355   360   365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln
    370   375   380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp
385   390   395   400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu
            405   410   415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe
            420   425   430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn
                        455/735

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            435                   440                   445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile
    450                   455                   460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp
465                   470                   475                   480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu
                485                   490                   495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser
                500                   505                   510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr
            515                   520                   525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn
            530                   535                   540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly
545                   550                   555                   560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln
                565                   570                   575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln
                580                   585                   590
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Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn
         595   600   605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe
     610   615   620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn
625   630   635   640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg
                 645   650   655

Leu Arg Ile Ser Glu Lys
             660

<210> 130

<211> 2251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(2059)

<400> 130

cttggctgga cagtttgtga aactgtgttg ccgggcaact ggacatcctt ttgttcaata 60

tcagtggttc aaa atg aat aaa gag att cca aat gga aat aca tca gag   109

```
                Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu
                 1                   5                   10


    ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt    157
    Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys
             15                  20                  25


    cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg    205
    Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu
             30                  35                  40


    gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc    253
    Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val
     45                  50                  55                  60


    tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg    301
    Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu
                     65                  70                  75


    atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct    349
    Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro
                     80                  85                  90


    att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag    397
    Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu
                     95                  100                 105


    acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga    445
    Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly
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        110                 115                 120


acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag    493
Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys
125                 130                 135                 140


aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act    541
Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr
                    145                 150                 155


gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca    589
Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr
                    160                 165                 170


act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat    637
Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn
                175                 180                 185


atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg    685
Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val
                190                 195                 200


tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca    733
Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser
205                 210                 215                 220


ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt    781
Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe
                    225                 230                 235
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tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga      829
Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly
            240             245             250


cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct      877
His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala
            255             260             265


cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg      925
Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu
            270             275             280


aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat      973
Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp
285             290             295             300


atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat     1021
Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp
            305             310             315


gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa     1069
Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln
            320             325             330


gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc     1117
Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile
            335             340             345
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ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act   1165
Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr
   350   355   360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc   1213
Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr
   365   370   375   380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga   1261
Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg
          385   390   395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt   1309
Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu
          400   405   410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg   1357
Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met
        415   420   425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct   1405
Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala
        430   435   440

gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca   1453
Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro
445   450   455   460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat   1501

                Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp
                        465   470   475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act   1549
Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr
            480   485   490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc   1597
Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr
        495   500   505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta   1645
Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val
    510   515   520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag   1693
Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys
525   530   535   540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat   1741
Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His
                545   550   555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat   1789
Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn
            560   565   570

ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat   1837
Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr
                    462/735

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                575                      580                          585


    cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt     1885
    His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly
        590                      595                      600


    aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act     1933
    Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr
    605                      610                      615                  620


    cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt     1981
    Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe
                        625                      630                      635


    agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt     2029
    Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser
                        640                      645                      650


    ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa       2079
    Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys
                655                      660


    gttagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt   2139


    gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc   2199


    aggactttga gatgttgaaa ttacattatt taattacaga cttcctcttt ct          2251
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<210> 131

<211> 824

<212> PRT

<213> Homo sapiens

<400> 131

Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala
1   5   10   15

Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg
            20   25   30

Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala
        35   40   45

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg
        50   55   60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
65   70   75   80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
                85   90   95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
                100   105   110

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
                115   120   125

Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val
   130   135   140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp
145   150   155   160

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile
           165   170   175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val
        180   185   190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val
        195   200   205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu
     210   215   220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro
225   230   235   240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
        245   250   255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
        260   265   270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr
                465/735

                    275   280   285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
        290   295   300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305   310   315   320

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
                    325   330   335

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
                    340   345   350

Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu
                    355   360   365

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu
        370   375   380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
385   390   395   400

Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
                    405   410   415

Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
                    420   425   430

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Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
      435   440   445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
      450   455   460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
465   470   475   480

Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
               485   490   495

Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
           500   505   510

Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
          515   520   525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
      530   535   540

Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545   550   555   560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
          565   570   575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
          580   585   590

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
          595   600   605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
          610   615   620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
625   630   635   640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
          645   650   655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
          660   665   670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
          675   680   685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
          690   695   700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705   710   715   720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
                    725   730   735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
                              468/735

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                740                    745                    750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
        755                    760                    765


Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
        770                    775                    780


Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
785                    790                    795                    800


Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser
                805                    810                    815


Asp Arg Leu Arg Ile Ser Glu Lys
                820
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<210> 132

<211> 2828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (165)..(2636)

<400> 132

ggggcgggga gcggacttcc tcctctgagg gccgtgccgc gctgccagat ttgttcttcc 60

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gcccctgcct ccgcggctcg gaggcgagcg gaaggtgccc cggggccgag gcccgtgacg 120


gggcgggcgg gagccccggc agtccggggt cgccggcgag ggcc atg tcg ctg ttg   176
                                                 Met Ser Leu Leu
                                                  1


ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg   224
Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro
 5                  10                  15                  20


ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg   272
Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro
                    25                  30                  35


ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc cgg   320
Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg
                40                  45                  50


ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc   368
Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg
                55                  60                  65


ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct   416
Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro
                70                  75                  80


gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt   464
Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly
```

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85   90   95   100

tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act   512
Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr
                    105   110   115

gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac   560
Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn
             120   125   130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc   608
Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys
             135   140   145

cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat   656
Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn
             150   155   160

aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg   704
Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val
165   170   175   180

cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc   752
His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe
             185   190   195

acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca   800
Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro
             200   205   210

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gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa     848
Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln
        215                 220                 225


atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg     896
Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu
        230                 235                 240


gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg     944
Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp
245                 250                 255                 260


ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg     992
Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met
                265                 270                 275


gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta    1040
Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val
                280                 285                 290


tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata    1088
Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile
        295                 300                 305


gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat    1136
Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn
        310                 315                 320
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ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg     1184
Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala
325             330             335             340


aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac     1232
Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His
                345             350             355


ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta     1280
Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu
                360             365             370


ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa     1328
Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu
            375             380             385


tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag     1376
Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys
            390             395             400


gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt     1424
Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe
405             410             415             420


ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct     1472
Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser
                425             430             435


gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa     1520
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Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys
      440   445   450

gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat   1568
Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn
      455   460   465

gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc   1616
Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala
   470   475   480

aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa   1664
Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu
485   490   495   500

atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa   1712
Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys
      505   510   515

gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt   1760
Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val
      520   525   530

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta   1808
Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu
      535   540   545

gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata   1856
Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile
                     474/735

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         550              555              560


cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg    1904
Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp
565              570              575              580


gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt    1952
Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys
                 585              590              595


ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg    2000
Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met
                 600              605              610


atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt    2048
Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys
                 615              620              625


gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa    2096
Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys
                 630              635              640


gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca    2144
Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser
645              650              655              660


aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa    2192
Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln
                 665              670              675
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```
aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac    2240
Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr
        680                 685                 690


tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg    2288
Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly
        695                 700                 705


aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag    2336
Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys
        710                 715                 720


act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct    2384
Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser
725                 730                 735                 740


gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca    2432
Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro
        745                 750                 755


ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca    2480
Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr
        760                 765                 770


cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca    2528
Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser
        775                 780                 785
```

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agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca    2576
Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro
        790             795             800


gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga    2624
Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg
805             810             815             820


att tct gaa aaa tgacctcctt gttttttgaaa gttagcataa ttttagatgc       2676
Ile Ser Glu Lys


ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736


gtagagaaag aatagtagta actgtttcat agcaaacttc aggactttga gatgttgaaa 2796


ttacattatt taattacaga cttcctcttt ct                               2828
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<210> 133

<211> 919

<212> PRT

<213> Homo sapiens

<400> 133

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Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn Glu Thr
1               5               10              15


Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser
            20              25              30
```

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys
        35   40   45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp
        50   55   60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys
        65   70   75   80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu
                        85   90   95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile
                        100   105   110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu
                115   120   125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu
        130   135   140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr
145   150   155   160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe
                165   170   175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr
                        478/735

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                180                      185                      190

    Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly
            195                      200                      205

    Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg
            210                      215                      220

    Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu
    225                      230                      235                      240

    Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr
                245                      250                      255

    Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr
                260                      265                      270

    Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly
                275                      280                      285

    Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala
            290                      295                      300

    Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu
    305                      310                      315                      320

    Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro
                325                      330                      335
```

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr
   340   345   350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser
   355   360   365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly
   370   375   380

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala
385   390   395   400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile
   405   410   415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala
   420   425   430

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg
   435   440   445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
   450   455   460

Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys
465   470   475   480

Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys
   485   490   495

Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln
            500   505   510

Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala
            515   520   525

Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile
            530   535   540

Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile
545   550   555   560

Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr
                565   570   575

Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln
                580   585   590

Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser
                595   600   605

Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His
            610   615   620

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala
625   630   635   640

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp
                            481/735

                645   650   655

Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala
              660   665   670

Ala Asp Met Ile Leu Val Asp Asp Phe Gln Thr Ile Met Ser Ala
              675   680   685

Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg
              690   695   700

Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala
705   710   715   720

Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp
                     725   730   735

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu
              740   745   750

Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp
              755   760   765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile
              770   775   780

Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp
785   790   795   800

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val
              805   810   815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser
              820   825   830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val
              835   840   845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu
              850   855   860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe
865   870   875   880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys
              885   890   895

Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr
              900   905   910

Ser Ser Ser Phe Leu Glu Val
              915

<210> 134

<211> 3612

<212> DNA

<213> Homo sapiens

483/735

<220>

<221> CDS

<222> (427)..(3183)

<400> 134

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cctccccgcc cgccctctct ccctcccttc ctccctcccg ctcgcttctt ctcacgccgg 120

gagcaggctc ccgcctcgca ccgctgcccc gcgagcagct cctcttctcc cgaggcgcgc 180

ggggcgcccc cgcgagcccc gcggctgaga ccccgcagcc tggaggaggg ctgtccgggg 240

ctttggatgc tgctgctagg ggtggtggga gcagccgtgg gacgcgtggc cgggagcggg 300

ggtgacagcc tgggattccg ggggcttctc ttccttgtcc tcctcctctc ctctctattc 360

ccagtgtggc cgtggctgac actaaagact tgtagccat caacccgagt gcagtttcga 420

tggaaa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat   468
       Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn
        1   5   10

gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca   516
Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro
15   20   25   30

gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta   564
Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu
484/735

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            Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu
                        35                  40                  45


            aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat ggc tgg aat gag    612
            Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu
                        50                  55                  60


            ttt gat att agt gaa gat gag cca ctg tgg aag aag tat att tct cag    660
            Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln
                        65                  70                  75


            ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt    708
            Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser
                    80                  85                  90


            gtt tta atg cat cag ttt gat gat gcc gtc agt atc act gtg gca ata    756
            Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile
                95                  100                 105                 110


            ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa    804
            Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys
                        115                 120                 125


            tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg    852
            Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val
                        130                 135                 140


            cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt    900
            Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly
                                        485/735
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                        145   150   155

gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc   948
Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg
        160   165   170

ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt   996
Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly
175   180   185   190

gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act   1044
Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr
                195   200   205

aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg   1092
Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu
                210   215   220

gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat   1140
Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn
                225   230   235

tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca   1188
Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro
        240   245   250

aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc   1236
Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser
255   260   265   270

ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta   1284
Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu
            275   280   285

ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct   1332
Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala
            290   295   300

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta   1380
Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu
            305   310   315

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag   1428
Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys
            320   325   330

ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat   1476
Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp
335   340   345   350

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt   1524
Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe
            355   360   365

act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa   1572
Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln
            370   375   380

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ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac    1620
Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn
        385               390               395


cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct    1668
Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala
        400               405               410


gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta    1716
Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu
415               420               425               430


att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac    1764
Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr
        435               440               445


atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct    1812
Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala
        450               455               460


gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt    1860
Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe
        465               470               475


atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag    1908
Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln
        480               485               490


agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac    1956
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Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr
495   500   505   510

caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct   2004
Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala
                515   520   525

ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg   2052
Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val
                530   535   540

gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca   2100
Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr
            545   550   555

ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag   2148
Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln
        560   565   570

gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act   2196
Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr
575   580   585   590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag   2244
Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln
                595   600   605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca   2292
Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro
                          489/735

agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt   2340
Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val
            625   630   635

gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct   2388
Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala
            640   645   650

gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa   2436
Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys
655   660   665   670

gag gca gca gac atg atc cta gtg gat gat gat ttt caa acc ata atg   2484
Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met
                    675   680   685

tct gca atc gaa gag ggt aaa ggg att tat aat aac att aaa aat ttc   2532
Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe
                    690   695   700

gtt aga ttc cag ctg agc acg agt ata gca gca tta act tta atc tca   2580
Val Arg Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser
            705   710   715

ttg gct aca tta atg aac ttt cct aat cct ctc aat gcc atg cag att   2628
Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile
            720   725   730

ttg tgg atc aat att att atg gat gga ccc cca gct cag agc ctt gga   2676
Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly
735   740   745   750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg   2724
Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp
              755   760   765

aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca   2772
Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser
              770   775   780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta   2820
Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu
              785   790   795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc   2868
Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys
    800   805   810

ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc   2916
Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr
815   820   825   830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat   2964
Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr
              835   840   845

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gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct     3012
Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro
            850             855             860


ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg     3060
Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu
            865             870             875


ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att     3108
Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile
            880             885             890


ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt     3156
Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser
895             900             905             910


tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt          3203
Ser Thr Ser Ser Ser Phe Leu Glu Val
            915


tatttgcaaa ctaggaattg cagtctgagg atcatttaga agggcaagtt caagaggata 3263


tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323


ttaagacttt aacctgctgg cagtcccaaa tgaaattatg caactttgat atcatattcc 3383


ttgatttaaa ttggcttttg tgattgagtg aaactttata aagcatatgg tcagttattt 3443


aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtacaaata 3503
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cactatctat cttagataga tatatttttt tttattttta aatattgtac tatttatggt 3563

ggtggggctt tcttactaat acacaaataa atttaatcat ttcaaaggc 3612

<210> 135

<211> 382

<212> PRT

<213> Homo sapiens

<400> 135

Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln
1   5   10   15

Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp
                20   25   30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser
            35   40   45

Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly
        50   55   60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr
65   70   75   80

Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn
                85   90   95

Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met
        100   105   110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr
        115   120   125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys
        130   135   140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe
145   150   155   160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln
            165   170   175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala
        180   185   190

Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys
        195   200   205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile
        210   215   220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly
225   230   235   240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser

```
                    245                      250                      255


Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val
                    260                      265                270


Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu
               275                      280                285


Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys
               290                      295                300


Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile
305                      310                      315                320


Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr
                    325                      330                335


Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala
                    340                      345                350


Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr
               355                      360                365


Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp
               370                      375                380
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<210> 136

<211> 2467

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (444)..(1589)

<400> 136

acgggagcgc gcgcgggagc tagagagcag tggtctcggc gctcgtccgg cccgcagctt 60

cgggtcctca ggcggctgtt gctccggaac gggtggttgg ggaggggggg gtggggggac 120

tctagacagc tgaggcgcga aagcgatgag tcctcggctc ttcctcctcc ttctccggga 180

cccgctctct gcctccctct ccaacgcccg gatgatctga gccgcgaggg cgccgacagc 240

cggggggcccg gacgcagccc ggctcctccc ctcctccgcc ccttccccag cctgacctgg 300

cccgccgctg cagcggtgac ccctcccccg gctgccgccg tcgccgccgc ggtgaccccc 360

tccccggctg ccgccgccgc cgcctcggcc gaccagggac ctgcccgcct gcggctgctc 420

cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg   473
                          Met Gly Ala Phe Leu Asp Lys Pro Lys Met
                          1   5   10

gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta   521
Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu
            15   20   25

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agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct    569
Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala
                30              35              40


gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg    617
Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val
                45              50              55


tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat    665
Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His
        60              65              70


ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga    713
Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly
    75              80              85              90


gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg    761
Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu
                95              100             105


gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca    809
Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala
                110             115             120


gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat    857
Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His
        125             130             135
```

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac   905
Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn
    140   145   150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg   953
Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu
155   160   165   170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt   1001
Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg
            175   180   185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac   1049
Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr
            190   195   200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag   1097
Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu
            205   210   215

cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att   1145
Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile
            220   225   230

atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc   1193
Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu
235   240   245   250

tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa   1241

Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys
              255   260   265

gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac   1289
Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp
              270   275   280

aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg   1337
Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser
              285   290   295

cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc   1385
Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys
              300   305   310

aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta   1433
Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu
315   320   325   330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca   1481
Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro
              335   340   345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac   1529
Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr
              350   355   360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca   1577
Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

<pre>
      365   370   375
</pre>

<pre>
gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc   1629
Asp Asp Met Trp
        380
</pre>

<pre>
aaaggagagt acagctcaac tttgttgaaa cttttaacat ccatcctcaa ctttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749

ccagaactga tttttttttt tttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaaat cagactccag caatttttgt tgtatgattt tgtttttttg 1869

taaagtgtaa ttgtccttgt acaaaatgct catatttaat tatgaactgc tttaaatcac 1929

tatcaaagtt acaagaaatg tttggcttat tgtgtgatgc aacagatata tagccctttc 1989

aagtcatgtt gtgtttggac ttggggttgg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaaat gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaaatgt tcttggtagg ggagttggca ttgttgataa 2169

agccagtccc ttcatttaac tgtctttcag gatgttcctt cgttgtttcc atgagtattg 2229

caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349
</pre>

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tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409


gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt   2467
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<210> 137

<211> 358

<212> PRT

<213> Homo sapiens

<400> 137

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Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val
 1               5                  10                  15


Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp
                20                  25                  30


Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu
                35                  40                  45


Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val
        50                  55                  60


Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg
65                  70                  75                  80


Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn
                85                  90                  95
```

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser
            100   105   110

Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser
            115   120   125

Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met
            130   135   140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala
145   150   155   160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser
                165   170   175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr
                180   185   190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln
            195   200   205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln
            210   215   220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro
225   230   235   240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln
                            502/735

                245   250   255

Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln
            260   265   270

Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr
            275   280   285

Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln
            290   295   300

Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly
305   310   315   320

Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro
            325   330   335

Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln
            340   345   350

Pro Gly Pro Gly Tyr Arg
            355

<210> 138

<211> 1519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11)..(1084)

<400> 138

| attagtgcta atg atg caa cga gtt ttc aga gga aaa ctt ctg agt aat | 49 |

          Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn

            1   5   10

| gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca | 97 |

Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr

     15   20   25

| att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata | 145 |

Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile

30   35   40   45

| ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca | 193 |

Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser

         50   55   60

| agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa | 241 |

Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys

         65   70   75

| gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct | 289 |

Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro

     80   85   90

```
tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag    337
Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys
     95              100              105


tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca    385
Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala
110              115              120              125


agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa    433
Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys
                 130              135              140


aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca    481
Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro
                 145              150              155


ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct    529
Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala
                 160              165              170


tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca    577
Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro
                 175              180              185


cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac    625
Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr
190              195              200              205


cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag    673
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505/735

```
Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln
             210                 215                 220


cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag     721
Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln
             225                 230                 235


act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca     769
Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro
         240                 245                 250


act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg     817
Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu
     255                 260                 265


cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa     865
Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln
270                 275                 280                 285


act tac act gcc caa act tct cag cct act aat tat act gtg gct cct     913
Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro
             290                 295                 300


gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca     961
Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro
             305                 310                 315


aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca    1009
Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro
```

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```
            320                 325                 330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc    1057
Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly
            335                 340                 345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc          1104
Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
350                 355
```

```
aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta 1164

ttgaagaagt tcagaaattt aaaagcagag catttttat gatatcattg ttggtgttaa 1224

ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tccctgctta 1284

aaaatgtagc agcttcttag ttactttgga acactactct tacatgtata aagtgattga 1344

cttgactttc tagcttccct tgtccggagg atattaaaat gctagggtga ggtttagcca 1404

tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa 1464

gatattatgt ataaaatgta acactgatga taggttaata aagatgattg aatcc        1519
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<210> 139

<211> 396

<212> PRT

<213> Homo sapiens

<400> 139

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln
1   5   10   15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr
            20   25   30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu
        35   40   45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp
        50   55   60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys
65   70   75   80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro
                85   90   95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu
                100   105   110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu
            115   120   125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg
            130   135   140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
145   150   155   160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
                165   170   175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val
                180   185   190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp
                195   200   205

Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro
                210   215   220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr
225   230   235   240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
                245   250   255

Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
                260   265   270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
                275   280   285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
                290   295   300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr
305   310   315   320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr
                325   330   335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala
                340   345   350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
            355   360   365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe
    370   375   380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
385   390   395

<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(1206)

<400> 140

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aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta      51
                    Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu
                    1               5                   10


atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat      99
Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His
            15                  20                  25


aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt     147
Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val
            30                  35                  40


ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa     195
Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys
            45                  50                  55


gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc     243
Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser
60                  65                  70                  75


ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat     291
Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn
            80                  85                  90


ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga     339
Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg
            95                  100                 105
```

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```
gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg   387
Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu
        110             115             120


gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat   435
Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp
        125             130             135


act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa   483
Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys
140             145             150             155


cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta   531
Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu
            160             165             170


aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta   579
Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu
            175             180             185


aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt   627
Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg
        190             195             200


tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca   675
Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro
205             210             215


cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa   723
```

```
Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln
220             225             230             235


gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca     771
Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala
                240             245             250


cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag     819
Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln
                255             260             265


tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag     867
Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln
                270             275             280


ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc     915
Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala
            285             290             295


ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac     963
Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
300             305             310             315


cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag    1011
Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln
                320             325             330


cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca    1059
Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro
```

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            335                 340                 345


agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct   1107
Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro
       350                 355                 360


gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt   1155
Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg
       365                 370                 375


aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat   1203
Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr
380                 385                 390                 395


cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc      1256
Arg


caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag   1316


cattttttat gatatcattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga   1376


ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga   1436


acactactct tacatgtata aagtgattga cttgactttc tagcttccct tgtccggagg   1496


atattaaaat gctagggtga ggtttagcca tcttacttgg ctttttacta ttaacatgat   1556


gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga   1616
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taggttaata aagatgattg aatcc   1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

1   5   10   15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr

                20   25   30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

            35   40   45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro

        50   55   60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly

65   70   75   80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly

                85   90   95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val

            100   105   110

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Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
         115                 120                 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
         130                 135                 140

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
145                 150                 155                 160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
                 165                 170                 175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
                 180                 185                 190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
             195                 200                 205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
         210                 215                 220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
225                 230                 235                 240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
                 245                 250                 255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
                 516/735
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                 260                    265                        270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
           275                    280                    285


Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
           290                    295                    300


Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
305                    310                    315                    320


Val Gln Thr
```

<210> 142

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)..(1040)

<400> 142

aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggt ggccacagag   60

gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca   110
            Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro

```
              1                 5                    10

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt    158
Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu
     15                  20                  25


cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt    206
Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe
 30                  35                  40                  45


gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac    254
Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His
                 50                  55                  60


ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg    302
Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg
                 65                  70                  75


cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc    350
Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe
                 80                  85                  90


cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat    398
Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp
     95                  100                 105


ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc    446
Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg
110                 115                 120                 125
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gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag   494

Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln

            130   135   140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg   542

Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro

            145   150   155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga   590

Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly

            160   165   170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc   638

Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro

            175   180   185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca   686

Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro

190   195   200   205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg   734

Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg

            210   215   220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac   782

Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn

            225   230   235

```
ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac    830
Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn
        240                 245                 250


tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc    878
Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val
        255                 260                 265


cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc    926
Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu
270                 275                 280                 285


aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg    974
Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu
                290                 295                 300


agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag    1022
Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln
                305                 310                 315


ctg acc cat gtg cag aca taggcggctt cctggccctg gggccggggg    1070
Leu Thr His Val Gln Thr
        320


ctggggtgtg gggcagtctg ggtcctctca tcatccccac ttcccaggcc cagcctttcc    1130


aaccctgcct gggatctggg ctttaatgca gaggccatgt ccttgtctgg tcctgcttct    1190


ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag    1250
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cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg 1310

agaggggagg agtgggcagt gaagatgaag ccccatgctc agtccctcc catcccccac 1370

gcagctccac cccagtccca agccaccagc tgtctgctcc tggtgggagg tggcctcctc 1430

agccctcct ctctgacctt taacctcact ctcaccttgc accgtgcacc aaccttcac 1490

ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac   1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
1   5   10   15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
                20   25   30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

```
              35                        40                        45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
        50                        55                        60


Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
    65                        70                        75                        80


Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
                    85                        90                        95


Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His
                    100                       105                       110


Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe
                    115                       120                       125


Leu Gln Pro Leu Met His Cys Val
        130                       135
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<210> 144

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(632)

<400> 144

acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa ggggggcgc aaaa atg gct ggg gca 236
                                                      Met Ala Gly Ala
                                                        1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att   284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
 5   10   15   20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct   332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
                 25   30   35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat   380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
             40   45   50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc   428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
         55   60   65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa   476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
                                       523/735

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          Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
               70                  75                  80


          att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac    524
          Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
           85                  90                  95                  100


          atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca    572
          Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser
                       105                 110                 115


          gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta    620
          Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu
                       120                 125                 130


          atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca    672
          Met His Cys Val
                       135


          ttgttaatta gtgacatagt aacatctgta gcagctggtt agtaaacctc atgtggggggt 732


          ggggtggggg tgtattcctt ggggggatggt ttgggccgaa tggggagtgg aatatttgac 792


          attttcctg ttttaaattc taggatagat tttaacatcc tttgcggtcc cagtccaagg 852


          taggctggtg tcatagtctt ctcactccta atccatgacc actgtttttt tcctatttat 912


          atcaccaggt agcctactga gttaatattt aagttgtcaa tagataagtg tccctgtttt 972
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gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta tttcagcttt 1032

gaaaccaaat ctgtgtatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092

ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152

tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212

gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
1   5   10   15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe
                20   25   30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln
            35   40   45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg
        50   55   60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro
65   70   75   80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu
                      85   90   95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser
                     100   105   110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu
                     115   120   125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu
                     130   135   140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met
145   150   155   160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp
                     165   170   175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val
                     180   185   190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu
                     195   200   205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp
210   215   220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile
225   230   235   240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala
                245   250   255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu
                260   265   270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe
                275   280   285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe
                290   295   300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys
305   310   315   320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser
                325   330   335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile
                340   345   350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met
                355   360   365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys
                        527/735

370   375   380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile
385   390   395   400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala
                        405   410   415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu
                        420   425   430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr
                        435   440   445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala
                        450   455   460

Ala Ser Gly Ile
465

<210> 146

<211> 1943

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (379)..(1782)

<400> 146

acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa ggggggggcgc aaaaatggct ggggcaatta 240

tagaaaacat gagcaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

tcatcgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt   411
                     Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly
                      1   5   10

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag   459
Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys
             15   20   25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc   507
Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe
         30   35   40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt   555
Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val
     45   50   55

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tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc    603
Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala
60              65              70              75


cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag    651
His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys
                80              85              90


act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc    699
Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe
            95              100             105


atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg    747
Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg
        110             115             120


ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata    795
Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile
        125             130             135


aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag    843
Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys
140             145             150             155


gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att    891
Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile
            160             165             170
```

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg   939
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val
             175   180   185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc   987
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile
            190   195   200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg   1035
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met
         205   210   215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg   1083
Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu
220   225   230   235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag   1131
Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu
            240   245   250

cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt   1179
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val
            255   260   265

ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa   1227
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln
            270   275   280

ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag   1275

Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu
    285   290   295

ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac   1323
Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr
300   305   310   315

ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt   1371
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser
                320   325   330

ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac   1419
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His
                335   340   345

tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg   1467
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu
        350   355   360

gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg   1515
Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr
        365   370   375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc   1563
Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala
380   385   390   395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg   1611
Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu
                    532/735

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                    400                    405                    410


atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc    1659
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser
            415                    420                    425


aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt    1707
Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe
            430                    435                    440


gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc    1755
Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe
            445                    450                    455


atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca          1802
Ile Asn Asp Asn Ala Ala Ser Gly Ile
460                    465


tgtttatcag ctttgcattt gcagttgtca cagtcacatt gattgtactt gtatacgcac   1862


acaaatacac tcatttagcc tttatctcaa aatgttaaat ataaggaaaa aagcgtcaac   1922


aataaatatt ctttgagtat t                                            1943
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<210> 147

<211> 460

<212> PRT

<213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
1   5   10   15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly
                20   25   30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro
            35   40   45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr
        50   55   60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr
65   70   75   80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val
                85   90   95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu
                100   105   110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
            115   120   125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
            130   135   140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
145   150   155   160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
            165   170   175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met
            180   185   190   .

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp
        195   200   205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala
    210   215   220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp
225   230   235   240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
                245   250   255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg
            260   265   270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile
        275   280   285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu
    290   295   300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg
305   310   315   320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg
            325   330   335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu
            340   345   350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser
            355   360   365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val
    370   375   380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val
385   390   395   400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu
            405   410   415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys
            420   425   430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys
            435   440   445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
                      536/735

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376)..(1755)

<400> 148

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gccttccgtc ccggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagcgccc 120

agaaaggagg cgaggaagga gggagtgtat gagaggaggg agcaaaaagc tcaccctaaa 180

acatttattt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tcgcctttct ggtgggaggc ttgattgctc cagggcccac aacggcagtg tcctacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411
              Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser
              1   5   10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg   459
Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg
          15   20   25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca   507
Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr
          30   35   40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt   555
Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe
     45   50   55   60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa   603
Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys
                  65   70   75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat   651
Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr
                  80   85   90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag   699
Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys
          95   100   105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc   747
Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile
          110   115   120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac   795

Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His
125   130   135   140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt   843
Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu
                145   150   155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc   891
Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr
                160   165   170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt   939
Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu
                175   180   185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc   987
Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile
                190   195   200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc   1035
Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly
205   210   215   220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag   1083
Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu
                225   230   235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag   1131
His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys

                240   245   250

caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac   1179
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp
        255   260   265

atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg   1227
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp
        270   275   280

act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct   1275
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala
285   290   295   300

gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt   1323
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe
                305   310   315

cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg   1371
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met
                320   325   330

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag   1419
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys
                335   340   345

ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc   1467
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe
                350   355   360

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ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc     1515
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile
365             370             375             380


aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg     1563
Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp
                385             390             395


aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa     1611
Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys
                400             405             410


aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg     1659
Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser
                415             420             425


agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc     1707
Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe
                430             435             440


agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att     1755
Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
445             450             455             460


tgagtcaaca aggcaacaca tgtttatcag ctttgcattt gcagttgtca cagtcacatt    1815


gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaat    1875
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ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc   1919

<210> 149

<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
1   5   10   15

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
            20   25   30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
            35   40   45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
        50   55   60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
65   70   75   80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
                85   90   95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
                100   105   110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
    115   120   125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
    130   135   140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145   150   155   160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
    165   170   175

Asp Arg His Lys Met Leu Ser
    180

<210> 150

<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120)..(668)

<400> 150

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ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc   119

atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc   167
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
1   5   10   15

cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc   215
Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
                20   25   30

tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta   263
Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
                35   40   45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg   311
Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
        50   55   60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac   359
Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
65   70   75   80

gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg   407
Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
                85   90   95

tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg   455
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
        100   105   110

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gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat        503
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
        115                 120                 125


gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc        551
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
    130                 135                 140


ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc        599
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145                 150                 155                 160


cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc        647
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
                165                 170                 175


gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc          698
Asp Arg His Lys Met Leu Ser
                180


ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt ctcccttccc     758


tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctccttctcc ctaactttag     818


aaatgttgta cttggctatt ttgattaggg aagagggatg tggtctctga tctccgttgt     878


cttcttgggt ctttgggggtt gaagggaggg ggaaggcagg ccagaaggga atggagacat    938
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545/735

tcgaggcggc ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 998

cagctctgag tcttgggaat gttgttaccc ttggaagata aagctgggtc ttcaggaact 1058

cagtgtctgg gaggaaagca tggcccagca ttcagcatgt gttcctttct gcagtggttc 1118

tttatcacca cctccctccc agccccagcg cctcagcccc agccccagct ccagccctga 1178

ggacagctct gatgggagag ctgggccccc tgagcccact gggtcttcag ggtgcactgg 1238

aagctggtgt tcgctgtccc ctgtgcactt ctcgcactgg ggcatggagt gcccatgcat 1298

actctgctgc cggtcccctc acctgcactt gaggggtctg ggcagtccct cctctcccca 1358

gtgtccacag tcactgagcc agacggtcgg ttggaacatg agactcgagg ctgagcgtgg 1418

atctgaacac cacagcccct gtacttgggt tgcctcttgt ccctgaactt cgttgtacca 1478

gtgcatggag agaaaatttt gtcctcttgt cttagagttg tgtgtaaatc aaggaagcca 1538

tcattaaatt gttttatttc tctc 1562

<210> 151

<211> 2815

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (192)..(2387)

<400> 151

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cagccaggtc tgtgctgccg ccctccagca tctttgcagc aggggacgag gctgtgtggg 120

aggctgtcgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggcttcatt 180

ctcccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc   230
              Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly
              1   5   10

att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag   278
Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys
    15   20   25

ctg ggg agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc   326
Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala
30   35   40   45

atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg   374
Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu
                50   55   60

gag tcc ttg aag atg aac aca gta gcc cag ctg gta gcc cac cag tgg   422
Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp
                65   70   75

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gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc      470
Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser
         80                  85                  90


tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt      518
Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys
         95                 100                 105


ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt      566
Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe
110                 115                 120                 125


gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg      614
Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp
                    130                 135                 140


gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca      662
Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro
                145                 150                 155


ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca      710
Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala
                160                 165                 170


gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg      758
Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp
                175                 180                 185
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gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac   806
Gly His Thr Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His
190   195   200   205

cta gag atc agc cag tca ccc act ctt gcc ttt ctc tct tca cac cat   854
Leu Glu Ile Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His
                210   215   220

gga acc cat ggg ccc agc aag cta tgt aac aca ccg ctg gac act cag   902
Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln
                225   230   235

gag cct cag ctt gtc cct gaa ggc tgc caa gaa cct gag gag ata agc   950
Glu Pro Gln Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser
                240   245   250

tgg cct cca tca gtg gag acc agt gtc tcc tta ggg tta cca cac gaa   998
Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu
                255   260   265

att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct   1046
Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro
270   275   280   285

gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc   1094
Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys
                290   295   300

aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa   1142

Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu
        305   310   315

agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt   1190
Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val
        320   325   330

cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct   1238
Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro
        335   340   345

gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct   1286
Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro
350   355   360   365

ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca acc tcc   1334
Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser
           370   375   380

aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat   1382
Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr
        385   390   395

aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt   1430
Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg
        400   405   410

att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc   1478
Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe

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                415                  420                       425


tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa    1526
Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln
430                 435                  440                  445


gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc    1574
Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser
                    450                  455                  460


ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac    1622
Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn
                    465                  470                  475


agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca    1670
Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro
                480                  485                  490


ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc    1718
Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu
        495                  500                  505


cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag    1766
His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys
510                  515                  520                  525


gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc    1814
Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg
                530                  535                  540
```

tgg aag aaa gcg cag gag gcc aga acc ctc aag gag cag agc ata cag   1862
Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln
           545   550   555

ctg gag gca gag cgg caa aac gtg gca gcc ata tct gct gcc tac aca   1910
Leu Glu Ala Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr
           560   565   570

gcc tat gtc cat agc tat agg gcc tgg caa gca gag atg aac aaa ctt   1958
Ala Tyr Val His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu
           575   580   585

ggg gtg gct ttt ggg aag aac ttg tca ctg ggg act cca aca ccc agc   2006
Gly Val Ala Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser
590   595   600   605

tgg ccc gga tgt cca cag cca ata cct tct cat cct cag ggt ggt act   2054
Trp Pro Gly Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr
               610   615   620

cca gtt ttc ccc tat tcc cca cag cct cca tcc ttc cct cag cct cca   2102
Pro Val Phe Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro
               625   630   635

tgc ttc cct cag cct cca tcc ttc cct cag cct cca tcc ttc cca ctg   2150
Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu
               640   645   650

cct cca gtc tct tcc cca cag tcc caa tcc ttt cca tca gcc tcc tcc   2198
Pro Pro Val Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser
    655   660   665

cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc   2246
Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala
670   675   680   685

cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg   2294
Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly
            690   695   700

gcc cag tca tct gat gac aag act gag tgt tcg gag aac ccc tgt atg   2342
Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met
            705   710   715

ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag   2387
Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
            720   725   730

tgaccaggtt ggaccccacc tagatggcta gagtgacaag attggacttc acctgggtcc 2447

ttaaaatgat agtggaggaa gggaacctcg cctgggtccc cagagtagcc agaggactta 2507

gcttgggctc ccacagtggc tattagttgg acccagcttg agaccccaga ggcagggaag 2567

accacaccta taaatcaggc ctgggaaaca tgcagaaacc ccatttgaac agactgtggg 2627

actccaatct gaatcctcta tgtggacaga ggatgatggg gccagaggca cctctgaggt 2687

gccctcagcg cagcctcgta aacttcattc actgtgacac atgctgttca tagggtctct 2747

ctggggagga tgcggtcccg gggcacatag ggagggtcct gtttttataa taaagttatt 2807

gacaactg   2815

<210> 152

<211> 732

<212> PRT

<213> Mus musculus

<400> 152

Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly Ile Leu Gly

1   5   10   15

Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys Leu Gly Ser

            20   25   30

Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu

        35   40   45

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu

    50   55   60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met

65   70   75   80

Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser Trp Thr Val
                85   90   95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser
               100   105   110

Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln
               115   120   125

Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys
               130   135   140

Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser
145   150   155   160

His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg
               165   170   175

Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr
               180   185   190

Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile
               195   200   205

Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His
               210   215   220

Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln
225   230   235   240

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Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser Trp Pro Pro
            245   250   255

Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu Ile Ser Val
            260   265   270

Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro Asp Ala Leu
            275   280   285

Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys Thr Glu Leu
            290   295   300

Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu Ser Val Gly
305   310   315   320

Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val Pro Val Gly
            325   330   335

Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro Ala Gln Pro
            340   345   350

Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro Leu Ser Ser
            355   360   365

Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser Thr Ser Pro
370   375   380

Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val
                      556/735

385   390   395   400

Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu
            405   410   415

Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu
            420   425   430

Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile
            435   440   445

Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys
            450   455   460

Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr
465   470   475   480

Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys
            485   490   495

Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile
            500   505   510

Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn
            515   520   525

Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys
            530   535   540

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Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala
545   550   555   560

Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val
                    565   570   575

His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala
                580   585   590

Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly
                595   600   605

Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe
                610   615   620

Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro
625   630   635   640

Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val
                    645   650   655

Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro
                660   665   670

Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val
                675   680   685

Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser
                690   695   700

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```
Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met Gly Pro Leu
705                 710                 715                 720


Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
                    725                 730
```

<210> 153

<211> 2544

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97)..(2232)

<400> 153

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tagggggacac tgggcgtgca gaaggcgggg ggcagtgtgg aacatgcctt caccacctcc   60


agcttctgct gccggaggct gcacccacct gtgccc atg gcc tgc aca ggc cca      114
                                          Met Ala Cys Thr Gly Pro
                                           1               5


tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag      162
Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys
           10                  15                  20
```

ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag   210
Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln
         25   30   35

ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa   258
Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu
         40   45   50

act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc   306
Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala
55   60   65   70

cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca   354
Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro
         75   80   85

gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg   402
Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu
         90   95   100

ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac   450
Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr
         105   110   115

cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg   498
Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly
       120   125   130

gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg   546

```
Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly
135             140             145             150
```

```
gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca    594
Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser Asn Leu Gly Cys Leu Pro
                155             160             165
```

```
cca tcc tcg gct ttg ccc tct ggg acc agg agc ctc cca cgc ccc att    642
Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg Ser Leu Pro Arg Pro Ile
                170             175             180
```

```
gac ggt gtt tcg gac tgg agc caa ggg tgc tcc ctg cga tcc act ggc    690
Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly
                185             190             195
```

```
agc cct gcc tcc ctg gcc agc aac ttg gaa atc agc cag tcc cct acc    738
Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu Ile Ser Gln Ser Pro Thr
        200             205             210
```

```
atg ccc ttc ctc agc ctg cac cgc agc cca cat ggg ccc agc aag ctc    786
Met Pro Phe Leu Ser Leu His Arg Ser Pro His Gly Pro Ser Lys Leu
215             220             225             230
```

```
tgt gac gac ccc cag gcc agc ttg gtg ccc gag cct gtc ccc ggt ggc    834
Cys Asp Asp Pro Gln Ala Ser Leu Val Pro Glu Pro Val Pro Gly Gly
                235             240             245
```

```
tgc cag gag cct gag gag atg agc tgg ccg cca tcg ggg gag att gcc    882
Cys Gln Glu Pro Glu Glu Met Ser Trp Pro Pro Ser Gly Glu Ile Ala
```

```
                  250                    255                      260


agc cca cca gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg      930
Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val
          265                    270                      275


gcc cca gat gca acc tcc act ggc ctc cct gat acc ccc gca gct cca      978
Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro
      280                    285                      290


gaa acc agc acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc     1026
Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly
295                    300                      305                  310


ccc cag tct ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc     1074
Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys
                  315                    320                      325


tct gtc aaa gac cag acg cca ctc caa ctt tct gta gaa gat acc acc     1122
Ser Val Lys Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr
              330                    335                      340


tct cca aat acc aag ccg tgc cca cct act ccc acc acc cca gaa aca     1170
Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr
          345                    350                      355


tcc cct cct cct cct cct cct cct cct tca tct act cct tgt tca gct     1218
Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala
      360                    365                      370
```

cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg   1266
His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser
375   380   385   390

gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa   1314
Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu
                 395   400   405

cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc   1362
His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro
                 410   415   420

gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag   1410
Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu
                 425   430   435

ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta   1458
Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu
        440   445   450

ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac   1506
Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn
455   460   465   470

caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc   1554
Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val
                 475   480   485

atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac   1602
Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp
        490   495   500

acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag   1650
Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln
        505   510   515

atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag   1698
Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln
        520   525   530

gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg   1746
Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg
535   540   545   550

gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg   1794
Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu
            555   560   565

aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca   1842
Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala
        570   575   580

cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg   1890
Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly
        585   590   595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc   1938

```
    Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro
        600                 605                 610


    ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg      1986
    Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro
    615                 620                 625                 630


    cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca      2034
    Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro
                    635                 640                 645


    cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc      2082
    Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala
                    650                 655                 660


    ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc      2130
    Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro
                    665                 670                 675


    ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac      2178
    Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His
        680                 685                 690


    atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag      2226
    Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu
    695                 700                 705                 710


    gca gaa tgaccgcgtg tccttgcctg accacctggg gaacacccct ggacccaggc      2282
    Ala Glu
```

atcggccagg acccccataga gcaccccggt ctgccctgtg ccctgtggac agtggaagat 2342

gaggtcatct gccactttca ggacattgtc cgggagccct tcatttagga caaaacgggc 2402

gcgatgatgc cctggctttc agggtggtca gaactggata cggtgtttac aattccaatc 2462

tctctatttc tgggtgaagg gtcttggtgg tggggggtatt gctacggtct tttaattata 2522

ataaatattt attgaatgct tc 2544

<210> 154

<211> 712

<212> PRT

<213> Homo sapiens

<400> 154

Met Ala Cys Thr Gly Pro Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly
1   5   10   15

Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys Thr
            20   25   30

Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu
        35   40   45

Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu
    50   55   60

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Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
65   70   75   80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
                       85   90   95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
                     100   105   110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
                   115   120   125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
                   130   135   140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
145   150   155   160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
                     165   170   175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
                   180   185   190

Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
                   195   200   205

Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
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                    210   215   220

His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro
225   230   235   240

Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro
                    245   250   255

Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro
                    260   265   270

Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro
                    275   280   285

Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys
                    290   295   300

Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu
305   310   315   320

Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu
                    325   330   335

Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr
                    340   345   350

Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser
                    355   360   365

                                    568/735

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
    370   375   380

Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu
385   390   395   400

His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu
          405   410   415

Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln
        420   425   430

Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
        435   440   445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu
        450   455   460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln
465   470   475   480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
          485   490   495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg
        500   505   510

Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
        515   520   525

Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln
      530   535   540

Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg
545   550   555   560

Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser
         565   570   575

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly
         580   585   590

Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro
         595   600   605

Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp
         610   615   620

Pro Gly Cys Pro Gln Pro Pro Leu His Ala Trp Gln Ala Gly Thr
625   630   635   640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro
         645   650   655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln
         660   665   670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln

                675   680   685

        Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala Pro
              690   695   700

        Glu Asp Lys Thr Gln Glu Ala Glu
        705   710

<210> 155

<211> 3456

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (281)..(3016)

<400> 155

agcattcaag gagctcccca ggagaaagag caagttctga ggagccctct gagcccggaa 60

cgtgtccacc cggtcatgcc cgccgcgcac cagccccgca gtggacttgg aggaggagga 120

ggaggagagc tctgtggatg gcaaagggga ccggaagagc acaggcctga aactctccaa 180

gaagaaagca aggaggagac acacggatga cccaagcaag gaatgcttca ctctgaaatt 240

tgacctgaat gtggacattg agacagagat cgtcccagcc atg aag aag aag tca   295

```
                                      Met Lys Lys Lys Ser
                                       1           5


ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg    343
Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu
             10              15              20


ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc    391
Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu
             25              30              35


acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc    439
Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala
             40              45              50


cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac    487
Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp
             55              60              65


tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc    535
Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro
 70              75              80              85


ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac    583
Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp
             90              95              100


atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg    631
Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly
```

```
              105                110                115


gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct     679
Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser
         120                125                130


ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag     727
Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys
         135                140                145


aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc     775
Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser
150                155                160                165


acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc     823
Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly
                   170                175                180


aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg     871
Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly
              185                190                195


ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag     919
Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu
         200                205                210


gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc     967
Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu
         215                220                225
```

att gat ggg cat gag aag ctg acc cgg cgg cag tgc cac cag cag gag   1015
Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu
230   235   240   245

gcg gtg tgg gag ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg   1063
Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu
                 250   255   260

cgg gtg atc atc aac ctg ttc ttg tgc tgc ctc ctg aac ctg caa gag   1111
Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu
                 265   270   275

tca ggg ctg ctg tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc   1159
Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile
                 280   285   290

ccg gag atc gcg cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg   1207
Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala
                 295   300   305

ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg   1255
Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly
310   315   320   325

gac ttc ctc aaa ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac   1303
Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr
                 330   335   340

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atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc   1351
Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly
       345   350   355

ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag   1399
Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu
       360   365   370

aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa   1447
Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys
       375   380   385

ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg   1495
Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu
390   395   400   405

agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc   1543
Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile
       410   415   420

ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag   1591
Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln
       425   430   435

cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc   1639
Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala
       440   445   450

tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag   1687
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Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys
        455   460   465

gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg   1735
Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro
470   475   480   485

gag gag acg cgg cag ctg ctg ctg gag ggg agc ctg agg atg aag gag   1783
Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu
                490   495   500

ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg   1831
Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu
            505   510   515

ctg ttg gtg acc aaa gca gtg aag aag gca gag agg acc agg gtc atc   1879
Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile
        520   525   530

agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac   1927
Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp
        535   540   545

cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta   1975
Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val
550   555   560   565

ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg   2023
Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp
                        576/735

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                 570                   575                   580

gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca      2071
Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala
             585                   590                   595


cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag      2119
Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu
             600                   605                   610


gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa      2167
Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
             615                   620                   625


ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg      2215
Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg
630                   635                   640                   645


aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc      2263
Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser
             650                   655                   660


acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc      2311
Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser
             665                   670                   675


tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc      2359
Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr
             680                   685                   690
```

```
tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg     2407
Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu
    695             700             705


ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac     2455
Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr
710             715             720             725


ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca     2503
Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro
                730             735             740


atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc     2551
Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser
            745             750             755


cct cca ccc tcg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg     2599
Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu
            760             765             770


agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc     2647
Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu
    775             780             785


cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc     2695
Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser
790             795             800             805
```

```
cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg      2743
Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg
            810               815               820


act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg      2791
Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly
            825               830               835


gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg      2839
Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly
            840               845               850


gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg      2887
Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly
            855               860               865


gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag      2935
Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln
870               875               880               885


cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg      2983
His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu
            890               895               900


ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gaggccccca   3036
Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
            905               910


agagtgccat tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc   3096
```

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ttcagctact gcctcctgta tgcatgagcc ggatgctggg caggatccct gcctacgccc 3156

gggcccgatt tgcgctttgc cggactggat ggagtggagg aggcccaggc cacagtacca 3216

ccccacctgc ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag 3276

tcttcagggc tgggctccta ggctgcccat cctacttcta ccctcactgg cctccagtgg 3336

gattcactcc tgccctgccc ccaccttccc agtcccacag gccacccctg gcttgggctg 3396

ggttctgtga agttacgtat ttattgagct tttggttctt ttataaagac ttgtctagac 3456

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<211> 912

<212> PRT

<213> Homo sapiens

<400> 156

Met Lys Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg

1   5   10   15

Lys Gly Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn

            20   25   30

Thr Pro Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr

        35   40   45

Leu Arg Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu
　　　50　　　　　　　　55　　　　　　　　60

Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro
65　　　　　　　　70　　　　　　　　75　　　　　　　　80

Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg
　　　　　　　85　　　　　　　　90　　　　　　　　95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met
　　　　　　100　　　　　　105　　　　　　110

Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr
　　　　　　115　　　　　　120　　　　　　125

Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr
　　　130　　　　　　135　　　　　　140

Gly Asp Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe
145　　　　　　150　　　　　　155　　　　　　160

Ser Ser Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met
　　　　　　165　　　　　　170　　　　　　175

Glu Gln Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro
　　　　　　180　　　　　　185　　　　　　190

Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu
　　　　　　195　　　　　　200　　　　　　205

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Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp
    210   215   220

Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln
225   230   235   240

Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser
            245   250   255

Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu
            260   265   270

Leu Asn Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg
            275   280   285

Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp
    290   295   300

Ala Ser Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala
305   310   315   320

Leu Leu Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser
            325   330   335

Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met
            340   345   350

Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr
                        582/735

```
                 355                      360                      365
```

Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser

```
        370                      375                      380
```

Asp Met Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu

```
   385                      390                      395                      400
```

Leu Lys Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala

```
                 405                      410                      415
```

Val Val Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn

```
                 420                      425                      430
```

Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val

```
                 435                      440                      445
```

Ser Arg Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val

```
        450                      455                      460
```

Asp Lys Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile

```
   465                      470                      475                      480
```

Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser

```
                 485                      490                      495
```

Leu Arg Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe

```
                 500                      505                      510
```

Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu
            515   520   525

Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys
            530   535   540

Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu
545   550   555   560

Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala
                    565   570   575

Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu
                    580   585   590

Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln
                595   600   605

Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu
            610   615   620

Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser
625   630   635   640

Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys
                    645   650   655

Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro
                    660   665   670
                                        584/735

```
Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser
        675                 680                 685


Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro
        690                 695                 700


Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser
705                 710                 715                 720


Met Asp Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe
                725                 730                 735


Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser
                740                 745                 750


Pro Arg Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr
                755                 760                 765


Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser
        770                 775                 780


Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr
785                 790                 795                 800


Pro Ser Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro
                805                 810                 815


Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser
                        585/735
```

```
                820                 825                 830

Trp Asp Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val
        835                 840                 845


Gly Cys Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly
        850                 855                 860


Asp Leu Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro
865                 870                 875                 880


Gly Val Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg
                885                 890                 895


Ile Arg Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
                900                 905                 910
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<210> 157

<211> 3609

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (152)..(3169)

<400> 157

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ggatgtatgt caccacgccg actgccagca gctgcaccgc cgggggcccc tcaacctctg 120

cgaggcctgt gacagcaagt ccacagcac c atg cat tat gat ggg cat gtc   172
                                         Met His Tyr Asp Gly His Val
                                            1   5

cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc   220
Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser
         10   15   20

acc cgg tca tgc ccg ccg cgc acc agc ccc gca gtg gac ttg gag gag   268
Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu
         25   30   35

gag gag gag gag agc tct gtg gat ggc aaa ggg gac cgg aag agc aca   316
Glu Glu Glu Glu Ser Ser Val Asp Gly Lys Gly Asp Arg Lys Ser Thr
   40   45   50   55

ggc ctg aaa ctc tcc aag aag aaa gca agg agg aga cac acg gat gac   364
Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp
            60   65   70

cca agc aag gaa tgc ttc act ctg aaa ttt gac ctg aat gtg gac att   412
Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile
            75   80   85

gag aca gag atc gtc cca gcc atg aag aag aag tca ctg ggg gag gtg   460
                                   587/735

```
            Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val
                    90              95              100

            ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac      508
            Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp
                    105             110             115

            atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc acc ttc gag gcc      556
            Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala
            120             125             130             135

            tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc cca gcc aag cct      604
            Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala Pro Ala Lys Pro
                            140             145             150

            gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg      652
            Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu
                        155             160             165

            agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc ccc gcc ctg gag      700
            Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu
                        170             175             180

            cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct      748
            Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro
                        185             190             195

            ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg gag gcg agc atc      796
            Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile
```

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        200   205   210   215

ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct ctg ccc agc ggc   844
Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser Leu Pro Ser Gly
                220   225   230

agc agt ggc agc acc aac act ggc gac agc tgg aag aac cgg gcg gcc   892
Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys Asn Arg Ala Ala
                235   240   245

agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc acc agc gcc ttt   940
Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe
                250   255   260

ggc cgg gag gta gac aag atg gag cag ctg gag ggc aag ctg cac acc   988
Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr
                265   270   275

tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg ctg cgc ttc gac   1036
Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly Leu Arg Phe Asp
280   285   290   295

cat gac tcc tgg gag gag gag tac gat gaa gac gag gat gag gac aat   1084
His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu Asp Glu Asp Asn
                300   305   310

gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat   1132
Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His
                315   320   325
</pre>

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```
gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag      1180
Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu
    330                 335                 340


ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc      1228
Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile
    345                 350                 355


aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg      1276
Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu
360                 365                 370                 375


tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc ccg gag atc gcg      1324
Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala
                380                 385                 390


cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag      1372
Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu
            395                 400                 405


aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa      1420
Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys
    410                 415                 420


ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac atc cgc tac tgc      1468
Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys
    425                 430                 435
```

```
atg gag gag gag ggc tgc atg gag tac atg cgc ggc ctg ctg cgc gac     1516
Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp
440             445             450             455


aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag aag cac cca cag     1564
Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu Lys His Pro Gln
                460             465             470


tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa ccc cac cag cgg     1612
Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg
                475             480             485


ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg agg aag acc gag     1660
Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu
                490             495             500


gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc ggc tcc gtg gag     1708
Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu
    505             510             515


cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg     1756
Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg
520             525             530             535


cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc tac gag gtg gtg     1804
Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val
                540             545             550


gaa agc agc agc gac gaa gtg gac aag ctc ctg aag gaa ttt ctg cac     1852
Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys Glu Phe Leu His
```

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Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys Glu Phe Leu His
        555   560   565


```
ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg gag gag acg cgg      1900
Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro Glu Glu Thr Arg
        570                 575                 580


cag ctg ctg ctg gag ggg agc ctg agg atg aag gag ggg aag gac agc      1948
Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu Gly Lys Asp Ser
        585                 590                 595


aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg ctg ttg gtg acc      1996
Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr
600                 605                 610                 615


aaa gca gtg aag aag gca gag agg acc agg gtc atc agg cca ccc ctg      2044
Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile Arg Pro Pro Leu
        620                 625                 630


ctc gtg gac aag att gtg tgc cgg gag cta cgg gac cct ggg tcc ttc      2092
Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp Pro Gly Ser Phe
        635                 640                 645


ctc ctt atc tac ctg aat gag ttt cac agt gct gta ggg gcc tac acg      2140
Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val Gly Ala Tyr Thr
        650                 655                 660


ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg gtg gac acc att      2188
Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp Val Asp Thr Ile
```

```
                665                 670                 675


tac aat gcc cag aac cag ctg caa cag ctg cgt gca cag gag ccc cca    2236
Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala Gln Glu Pro Pro
680                 685                 690                 695


ggc agt cag cag ccc ctg cag agc ctg gaa gag gag gag gat gag cag    2284
Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu Glu Asp Glu Gln
                    700                 705                 710


gag gag gaa gag gag gag gag gag gag gag gag gaa ggc gag gac agt    2332
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Glu Asp Ser
                    715                 720                 725


ggc act tca gct gcc agc tcc cct acc atc atg cgg aaa agc agc ggc    2380
Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg Lys Ser Ser Gly
                    730                 735                 740


agc ccc gac tct cag cac tgt gcc tca gat ggc tcc acg gag acc ctg    2428
Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser Thr Glu Thr Leu
                    745                 750                 755


gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc tcc ccc gag ttc    2476
Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser Ser Pro Glu Phe
760                 765                 770                 775


gac agc ggt cct ttc agc tcc cag tct gat gag acc tct ctc agc acc    2524
Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr Ser Leu Ser Thr
                    780                 785                 790
```

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```
act gcc tca tct gcc acg ccc acc agt gag ctg ctg ccc ctg ggt ccg    2572
Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro
        795             800             805


gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac ggc acc ctc tcc    2620
Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr Gly Thr Leu Ser
        810             815             820


cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta    2668
Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro Met Ala Glu Leu
        825             830             835


gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc cct cca ccc tcg    2716
Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser
840             845             850             855


ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg agc tgc ccg ccc    2764
Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro
            860             865             870


cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc cag ctg ctg gca    2812
His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala
            875             880             885


ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc cgc agc ctg tca    2860
Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser Arg Ser Leu Ser
        890             895             900
```

```
gag ctc tgc ctg gct gtt cca gcc cca ggt att agg act cag ggc tcc     2908
Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg Thr Gln Gly Ser
    905             910             915


cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg gcc cct agc cct     2956
Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly Ala Pro Ser Pro
920             925             930                 935


ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg gaa cct gca ggc     3004
Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly Glu Pro Ala Gly
            940             945             950


tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg gcc tct ccc agg     3052
Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly Ala Ser Pro Arg
            955             960             965


gtc cag cct gag ccc cca cca ggg gtc tct gcc cag cac agg aag ctg     3100
Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln His Arg Lys Leu
            970             975             980


acc ctg gcc cag ctc tac cga atc agg acc acc ctg ctg ctt aac tcc     3148
Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser
    985             990             995


acg ctc act gcc tcg gag gtc tgagcagagg gaggcccccca agagtgccat       3199
Thr Leu Thr Ala Ser Glu Val
1000            1005


tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc ttcagctact 3259
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gcctcctgta tgcatgagcc ggatgctggg caggatccct gcctacgccc gggcccgatt 3319

tgcgctttgc cggactggat ggagtggagg aggcccaggc cacagtacca ccccacctgc 3379

ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag tcttcagggc 3439

tgggctccta ggctgcccat cctacttcta ccctcactgg cctccagtgg gattcactcc 3499

tgccctgccc ccaccttccc agtcccacag gccacccctg gcttgggctg ggttctgtga 3559

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<210> 158

<211> 1006

<212> PRT

<213> Homo sapiens

<400> 158

Met His Tyr Asp Gly His Val Arg Phe Asp Leu Pro Pro Gln Gly Ser
1   5   10   15

Val Leu Ala Arg Asn Val Ser Thr Arg Ser Cys Pro Pro Arg Thr Ser
                20   25   30

Pro Ala Val Asp Leu Glu Glu Glu Glu Glu Glu Ser Ser Val Asp Gly
                35   40   45

Lys Gly Asp Arg Lys Ser Thr Gly Leu Lys Leu Ser Lys Lys Lys Ala
50   55   60

Arg Arg Arg His Thr Asp Asp Pro Ser Lys Glu Cys Phe Thr Leu Lys
65   70   75   80

Phe Asp Leu Asn Val Asp Ile Glu Thr Glu Ile Val Pro Ala Met Lys
                85   90   95

Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly
                100   105   110

Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro
            115   120   125

Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg
            130   135   140

Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly
145   150   155   160

Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly
                165   170   175

Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu
                180   185   190

Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu
                195   200   205

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Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser
    210   215   220

Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp
225   230   235   240

Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser
           245   250   255

Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln
         260   265   270

Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu
         275   280   285

Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp
    290   295   300

Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp
305   310   315   320

Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His
           325   330   335

Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile
         340   345   350

Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn
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                    355   360   365

Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe
             370   375   380

Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser
385   390   395   400

Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu
                    405   410   415

Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe
                    420   425   430

Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr
                    435   440   445

Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr
             450   455   460

Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met
465   470   475   480

Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys
                    485   490   495

Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val
                    500   505   510

Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys
        515   520   525

Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg
        530   535   540

Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys
545   550   555   560

Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly
        565   570   575

Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg
        580   585   590

Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe
        595   600   605

Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr
        610   615   620

Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu
625   630   635   640

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His
        645   650   655

Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys
        660   665   670

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Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln
        675   680   685

Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu
        690   695   700

Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu
705   710   715   720

Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr
                725   730   735

Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser
                740   745   750

Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp
                755   760   765

Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser
        770   775   780

Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser
785   790   795   800

Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp
                805   810   815

Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala
                        601/735

```
            820                825                830

Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg
        835                840                845

Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val
        850                855                860

Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala
865                870                875                880

Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser
                885                890                895

Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro
                900                905                910

Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp
                915                920                925

Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys
        930                935                940

Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu
945                950                955                960

Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val
                965                970                975
```

Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg
            980   985   990

Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
            995   1000   1005

<210> 159

<211> 3168

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (93)..(3089)

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cactggcgcg atgcgggccg tcctctcggc tg atg ggt tgg aag ccc agc gag   113
                                     Met Gly Trp Lys Pro Ser Glu
                                      1   5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg   161
Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg
         10   15   20

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga   209

Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg

     25   30   35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg   257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val

     40   45   50   55

ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac   305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp

               60   65   70

ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc   353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly

           75   80   85

agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc   401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly

         90   95   100

acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg   449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu

   105   110   115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt   497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
120   125   130   135

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt   545
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg

```
                140                    145                      150


gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag    593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys
            155                    160                      165


cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc    641
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg
            170                    175                      180


cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg    689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg
            185                    190                      195


ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg    737
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp
200                    205                    210                      215


ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc    785
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile
            220                    225                      230


cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg    833
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp
            235                    240                      245


gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg    881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val
            250                    255                      260
```

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```
gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac     929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp
    265                 270                 275


cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt     977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser
280                 285                 290                 295


gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg    1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu
                300                 305                 310


gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac    1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn
                315                 320                 325


ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc    1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile
    330                 335                 340


acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg    1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp
    345                 350                 355


acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc    1217
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly
360                 365                 370                 375
```

```
gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag      1265
Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln
            380                 385                 390


gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc      1313
Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg
            395                 400                 405


gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca      1361
Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala
            410                 415                 420


gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac      1409
Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr
            425                 430                 435


cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag      1457
Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu
440                 445                 450                 455


aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag      1505
Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys
            460                 465                 470


agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt      1553
Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly
            475                 480                 485


aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg      1601
```

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Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val
     490   495   500

gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg   1649
Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu
     505   510   515

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg   1697
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val
     520   525   530   535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg   1745
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu
               540   545   550

ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg   1793
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg
               555   560   565

gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg   1841
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val
          570   575   580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt   1889
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys
     585   590   595

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc   1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala
                         608/735

600   605   610   615

```
atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag    1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
                620                 625                 630


gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg    2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
                635                 640                 645


ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att    2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
                650                 655                 660


ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc    2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
                665                 670                 675


acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag    2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
680                 685                 690                 695


atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag    2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys
                700                 705                 710


ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg    2273
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu
                715                 720                 725
```

```
gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag      2321
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu
        730                 735                 740


gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg      2369
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu
        745                 750                 755


ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg      2417
Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu
760                 765                 770                 775


ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg      2465
Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr
                780                 785                 790


gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg      2513
Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val
        795                 800                 805


agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag      2561
Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu
        810                 815                 820


ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag      2609
Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu
        825                 830                 835
```

```
cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg    2657
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
840             845             850             855
```

```
acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc    2705
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
                860             865             870
```

```
gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg    2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu
            875             880             885
```

```
ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg    2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
                890             895             900
```

```
atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc    2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg
        905             910             915
```

```
cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg    2897
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
920             925             930             935
```

```
cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa    2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu
            940             945             950
```

```
cgc atc acc tgc ccc atc tgc atc gac agg cac atc cgc ctc gtg ttc    2993
```

Arg Ile Thr Cys Pro Ile Cys Ile Asp Arg His Ile Arg Leu Val Phe
       955   960   965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc   3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala
       970   975   980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg   3089
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
       985   990   995

tgagccgcgc cgtccgccgc gcccgagctg ccttcgcgtg cccccgccct gtgttttata 3149

aaaagaaaga ttctcggat   3168

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<211> 999

<212> PRT

<213> Homo sapiens

<400> 160

Met Gly Trp Lys Pro Ser Glu Ala Arg Gly Gln Ser Gln Ser Leu Gln
1   5   10   15

Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr
       20   25   30

Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp

```
            35                    40                    45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
         50                    55                    60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
         65                    70                    75              80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
                   85                    90                    95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
                  100                   105                   110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
                  115                   120                   125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
                  130                   135                   140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
145                   150                   155                   160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
                  165                   170                   175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
                  180                   185                   190
```

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Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val
        195   200   205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys
        210   215   220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg
225   230   235   240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg
                245   250   255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala
                260   265   270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala
        275   280   285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly
        290   295   300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln
305   310   315   320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln
                325   330   335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
                340   345   350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
        355   360   365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu
        370   375   380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
385   390   395   400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly
                405   410   415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
                420   425   430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
        435   440   445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu
        450   455   460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
465   470   475   480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
                485   490   495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala
                        615/735

```
        500                   505                   510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
        515                   520                   525


Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
        530                   535                   540


Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
545                   550                   555                   560


Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
                565                   570                   575


Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
                580                   585                   590


Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
                595                   600                   605


Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
        610                   615                   620


Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
625                   630                   635                   640


Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
                645                   650                   655
```

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
        660   665   670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
        675   680   685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
        690   695   700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
705   710   715   720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
                725   730   735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
        740   745   750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
        755   760   765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
        770   775   780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
785   790   795   800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
        805   810   815

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Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
          820   825   830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
          835   840   845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
          850   855   860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
865   870   875   880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
                    885   890   895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
          900   905   910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
          915   920   925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
          930   935   940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
945   950   955   960

Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
                    618/735

```
          965                970                975
```

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg

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              980                985                990
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Asp Arg Ile Gln Ile Phe Val

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          995
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<400> 161

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cactggcgcg atgcgggccg tcctctcggc tg atg ggt tgg aag ccc agc gag   113

                                               Met Gly Trp Lys Pro Ser Glu

                                                1   5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg   161

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

      10   15   20

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga   209
Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
        25   30   35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg   257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val
    40   45   50   55

ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac   305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
                60   65   70

ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc   353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
            75   80   85

agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc   401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
        90   95   100

acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg   449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
        105   110   115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt   497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
120   125   130   135

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt   545
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg
              140   145   150

gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag   593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys
              155   160   165

cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc   641
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg
              170   175   180

cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg   689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg
              185   190   195

ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg   737
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp
200   205   210   215

ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc   785
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile
              220   225   230

cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg   833
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp
              235   240   245

gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg   881

Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val
        250   255   260

gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac   929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp
        265   270   275

cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt   977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser
280   285   290   295

gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg   1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu
                300   305   310

gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac   1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn
            315   320   325

ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc   1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile
            330   335   340

acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg   1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp
            345   350   355

acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc   1217
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly

```
gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag     1265
Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln
                380                  385                  390
```

```
gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc     1313
Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg
                395                  400                  405
```

```
gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca     1361
Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala
                410                  415                  420
```

```
gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac     1409
Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr
                425                  430                  435
```

```
cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag     1457
Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu
440                  445                  450                  455
```

```
aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag     1505
Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys
                460                  465                  470
```

```
agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt     1553
Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly
                475                  480                  485
```

```
aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg     1601
Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val
        490                 495                 500


gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg     1649
Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu
        505                 510                 515


ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg     1697
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val
520                 525                 530                 535


gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg     1745
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu
                540                 545                 550


ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg     1793
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg
            555                 560                 565


gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg     1841
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val
        570                 575                 580


cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt     1889
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys
        585                 590                 595
```

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc   1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala
600   605   610   615

atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag   1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
                620   625   630

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg   2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
                635   640   645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att   2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
                650   655   660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc   2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
                665   670   675

acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag   2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
680   685   690   695

atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag   2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys
                700   705   710

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg   2273

Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu
        715   720   725

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag   2321
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu
        730   735   740

gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg   2369
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu
        745   750   755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg   2417
Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu
760   765   770   775

ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg   2465
Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr
           780   785   790

gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg   2513
Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val
        795   800   805

agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag   2561
Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu
        810   815   820

ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag   2609
Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu

```
                825                    830                    835


cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg      2657
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
840                   845                    850                    855


acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc      2705
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
                          860                    865                    870


gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg      2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu
                     875                    880                    885


ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg      2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
                890                    895                    900


atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc      2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg
905                   910                    915


cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg      2897
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
920                   925                    930                    935


cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa      2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu
                940                    945                    950
```

```
cgc atc acc tgc ccc atc tgc atc gac agc cac atc cgc ctc gtg ttc   2993
Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe
        955                 960                 965


cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc   3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala
        970                 975                 980


tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg   3089
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
        985                 990                 995


tgagccgcgc cgtccgccgc gcccgagctg ccttcgcgtg cccccgccct gtgttttata 3149


aaaagaaaga ttctcggat                                               3168
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<210> 162

<211> 999

<212> PRT

<213> Homo sapiens

<400> 162

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Met Gly Trp Lys Pro Ser Glu Ala Arg Gly Gln Ser Gln Ser Leu Gln
1               5                   10                  15


Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr
        20                  25                  30
```

Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp
        35   40   45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
        50   55   60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
    65   70   75   80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
                85   90   95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
            100   105   110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
        115   120   125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
    130   135   140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
145   150   155   160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
                165   170   175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
                        629/735

                180   185   190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val
        195   200   205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys
        210   215   220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg
225   230   235   240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg
                245   250   255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala
                260   265   270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala
                275   280   285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly
        290   295   300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln
305   310   315   320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln
                325   330   335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
      340   345   350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
      355   360   365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu
      370   375   380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
385   390   395   400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly
      405   410   415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
      420   425   430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
      435   440   445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu
      450   455   460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
465   470   475   480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
      485   490   495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala
          500   505   510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
          515   520   525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
          530   535   540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
545   550   555   560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
          565   570   575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
          580   585   590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
          595   600   605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
          610   615   620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
625   630   635   640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
                         632/735

```
          645                    650                    655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
             660                    665                    670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
             675                    680                    685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
             690                    695                    700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
705                    710                    715                    720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
                       725                    730                    735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
             740                    745                    750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
             755                    760                    765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
770                    775                    780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
785                    790                    795                    800
```

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
            805   810   815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
            820   825   830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
            835   840   845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
            850   855   860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
865   870   875   880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
            885   890   895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
            900   905   910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
            915   920   925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
            930   935   940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
945   950   955   960

```
Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
            965                 970                 975


Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg
            980                 985                 990


Asp Arg Ile Gln Ile Phe Val
            995
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<210> 163

<211> 4031

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (91)..(2649)

<400> 163

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gttctggtcc cggtgagatg ctggaagctg ctgcggcagc cgcaacgcgc ccggtcgccg  60


tcccgtcgcc aatccccgcc gtcccgggcc atg atc gcc tgg cgt ctg ccc ttg  114
                                    Met Ile Ala Trp Arg Leu Pro Leu
                                     1                   5


tgc gtg ctc ttg gtg gcc tcc gtc gag agc cac ctg ggg gcc ctg ggg   162
```

```
Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly
         10                  15                  20
```

```
ccc aag aac gtc tcg cag aaa gac gcg gag ttt gag cgc acc tac gcg    210
Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala
 25                  30                  35                  40
```

```
gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc    258
Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr
                 45                  50                  55
```

```
gtg acc cgc aac cgg acc gag ggt gtg cga gtg tct gtg aat gtc ctg    306
Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu
                 60                  65                  70
```

```
aac aag cag aaa ggg gcg cct ttg ctg ttc gtg gtc cgc cag aag gag    354
Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu
                 75                  80                  85
```

```
gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag    402
Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln
         90                  95                 100
```

```
cgg aag tac ctc tac caa aaa gtg gaa cga act ctg tgt cag ccc ccc    450
Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
105                 110                 115                 120
```

```
acc aag aat gag tct gag atc cag ttt ttc tat gtg gac gtg tct acc    498
Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr
```

                    125   130   135

ctg tca ccc gtc aat acc act tac cag ctc cga gtc aac cgt gtg gac   546
Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Asn Arg Val Asp
            140   145   150

aat ttt gtg ctc agg act gga gag ctg ttt acc ttt aat acc act gca   594
Asn Phe Val Leu Arg Thr Gly Glu Leu Phe Thr Phe Asn Thr Thr Ala
            155   160   165

gcc cag ccc cag tac ttc aaa tac gag ttt cct gat ggt gtg gac tcg   642
Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Asp Gly Val Asp Ser
         170   175   180

gta att gtc aag gtg acc tcc aag aag gcc ttc ccc tgc tca gtc atc   690
Val Ile Val Lys Val Thr Ser Lys Lys Ala Phe Pro Cys Ser Val Ile
185   190   195   200

tcc atc cag gat gtc ctg tgc cct gtc tat gat ctg gac aac agt gta   738
Ser Ile Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Ser Val
                205   210   215

gcc ttc att ggc atg tac cag acg atg act aag aag gca gcc atc act   786
Ala Phe Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr
            220   225   230

gtg cag cgg aaa gac ttc ccc agc aac agc ttc tat gtg gtg gtg gta   834
Val Gln Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val
         235   240   245

gtg aag act gag gac cag gcc tgc gga ggg tcc ttg ccc ttc tac cct   882
Val Lys Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro
    250   255   260

ttt gtg gaa gat gag cca gtg gat caa ggg cac cgt cag aaa aca ctg   930
Phe Val Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu
265   270   275   280

tca gtg ctg gtc tct cag gct gtc aca tct gag gcc tat gtt ggt ggg   978
Ser Val Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Gly Gly
                 285   290   295

atg ctc ttt tgc ctg ggc ata ttc ttg tcc ttc tac ctg ctg act gtg   1026
Met Leu Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val
                 300   305   310

ctg ctg gcc tgt tgg gag aac tgg agg caa agg aag aag acc ttg ctg   1074
Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Arg Lys Lys Thr Leu Leu
                 315   320   325

gtg gcc ata gac cga gcc tgc cca gaa agt ggt cac gct cgg gtc ttg   1122
Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Ala Arg Val Leu
    330   335   340

gct gat tca ttt cct ggc agt gcc cct tac gag ggt tac aac tat ggc   1170
Ala Asp Ser Phe Pro Gly Ser Ala Pro Tyr Glu Gly Tyr Asn Tyr Gly
345   350   355   360

```
tcc ttt gaa aat ggt tcc gga tcc act gac ggg ttg gtt gaa agc gca      1218
Ser Phe Glu Asn Gly Ser Gly Ser Thr Asp Gly Leu Val Glu Ser Ala
            365                 370                 375


ggt tca ggg gac ctc tcc tac agt tac cag ggg cac gac cag ttc aag      1266
Gly Ser Gly Asp Leu Ser Tyr Ser Tyr Gln Gly His Asp Gln Phe Lys
            380                 385                 390


cgg cgc ctt ccc tct ggc cag atg cgg cag ctg tgc att gcc atg gac      1314
Arg Arg Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Asp
            395                 400                 405


cgc tcc ttt gac gca gtg ggt cct cgg cct cga ctg gac tcc atg agc      1362
Arg Ser Phe Asp Ala Val Gly Pro Arg Pro Arg Leu Asp Ser Met Ser
            410                 415                 420


tcc gtg gaa gag gat gac tac gac acg ctg act gac atc gac tca gac      1410
Ser Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp
425                 430                 435                 440


aaa aac gtc att cga acc aag caa tac ctc tgt gtg gct gat ctg gca      1458
Lys Asn Val Ile Arg Thr Lys Gln Tyr Leu Cys Val Ala Asp Leu Ala
            445                 450                 455


cga aag gac aaa cgt gtt ttg cgg aaa aag tac cag att tac ttc tgg      1506
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp
            460                 465                 470


aac ata gcc acc att gcg gtc ttc tac gca ctt cct gtg gtg cag ctg      1554
```

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```
Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu
    475             480             485
```

```
gtg atc acc tac cag acg gtg gtg aat gtc aca ggg aac cag gac atc        1602
Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile
    490             495             500
```

```
tgc tac tac aac ttc ctc tgt gcc cac ccg ctg ggc aac ctc agc gcc        1650
Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala
505             510             515             520
```

```
ttc aac aac atc ctc agc aac ttg ggg tac atc ctg ctg ggg ctg ctc        1698
Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu
                525             530             535
```

```
ttc ctg ctc atc atc ctg cag cga gag atc aat cat aac cgg gcc ctg        1746
Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu
        540             545             550
```

```
ctg cgg aat gac ctc tat gct ctg gag tgt ggg atc ccc aaa cac ttt        1794
Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe
        555             560             565
```

```
ggt ctg ttt tac gcc atg ggc aca gca ctg atg atg gag ggg cta ctt        1842
Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu
    570             575             580
```

```
agt gcc tgt tac cac gtc tgc ccc aac tac acc aac ttc cag ttt gat        1890
Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp
```

585   590   595   600

acc tcc ttc atg tac atg att gct ggc ctc tgc atg ctg aag ctc tac   1938
Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr
                  605   610   615

cag aag cgg cac cca gat atc aac gcc agt gcc tac agt gca tat gcc   1986
Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala
                  620   625   630

tgc ttg gcc atc gtc atc ttc ttc tcc gtt ctg ggc gtg gtg ttt ggc   2034
Cys Leu Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly
                  635   640   645

aaa ggg aac acg gcc ttc tgg att gtc ttc tcc gtc att cac atc atc   2082
Lys Gly Asn Thr Ala Phe Trp Ile Val Phe Ser Val Ile His Ile Ile
                  650   655   660

tcc acc ctg ctc ctc agc act cag ctc tat tac atg ggc cgc tgg aag   2130
Ser Thr Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys
665   670   675   680

ctg gac ttc ggg atc ttc cgc cgc atc ctc cat gtg ctc tac aca gac   2178
Leu Asp Phe Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
                  685   690   695

tgc atc cgg cag tgc agc ggg ccc ctt tac acg gac cgc atg gtg ctt   2226
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Thr Asp Arg Met Val Leu
                  700   705   710

ctg gtc atg ggc aac att atc aac tgg tcg ctg gct gca tac gga ctc   2274
Leu Val Met Gly Asn Ile Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu
            715   720   725

atc atg cgc ccc aat gac ttt gct tcc tac ttg ctg gca att ggc atc   2322
Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile
            730   735   740

tgc aac ctg ctg ctt tat ttc gcc ttc tac atc atc atg aag ctc cgg   2370
Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg
745   750   755   760

agc ggc gag agg atc aag ctc atc cct ctg ctt tgc atc gtc tgc acc   2418
Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr
            765   770   775

tcc gtg gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctg agc   2466
Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser
            780   785   790

acg tgg cag aaa acc ccc gca gag tcc agg gag cac aac cgc gac tgc   2514
Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys
            795   800   805

atc ctc ctc gac ttc ttt gat gac cac gat atc tgg cac ttc ctg tcc   2562
Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser
            810   815   820

```
tcc att gcc atg ttt ggg tcc ttc ctg gtt ttg ctg acg ttg gat gac      2610
Ser Ile Ala Met Phe Gly Ser Phe Leu Val Leu Leu Thr Leu Asp Asp
825                 830             835             840


gac ttg gac aca gta cag cgg gac aag atc tat gtc ttc tagcagcatc      2659
Asp Leu Asp Thr Val Gln Arg Asp Lys Ile Tyr Val Phe
                845                 850
```

```
tgtggtccag gcttcacctc acgggcctag cgcctgcctc tgcatcacct gccagttgcc 2719


acaagaacac cacgggtgtg agtcccagct ctgctgccca gcattggatg tcgtggcaag 2779


acagcgagat tccagcccag gcctgactca ggacagttcc tggtggcact gagccttgga 2839


gttgcctctg cggaggagga ggcctgctcc gcattcccca gacactggcc aaattgctgc 2899


tttcttctca gtgttgggtc ctccccagga ccctagtctg tccatctgtc ttgtttatcc 2959


actggctctc catttgtccc tttggagagg aaggtgggaa ggcaatgtcc tgtcccattt 3019


catgccttgc attctgccca tcccttccct cctctcagct taggacacac agccctttct 3079


tcttcccatg ctctgtccag gaccacagtc tggtgcctga ttctttgtcc atcaccagga 3139


cctaagctct ccctgggtct gtagctggct gctatcactg cccactctga cctgccagga 3199


cagatgcagg taggagactt tgggggctgg ccagctggtg ccaggctttc ggtgctaagg 3259


cctggaaggg gcctaggtac gaccctcctc cctgacctgt gcttggagct ggctcttcag 3319
```

```
cagtgagggc cagcccaagt tgagtcttct gatcggggac tgaattcaga ggccacctca 3379

tcccaccagc cactagaatg atgccagcac tagggttggt gggaagtggc aactcactgt 3439

cccctttccac accctcagtc ctgccaagcc ccagatgggg gcctctcagt gccattgaca 3499

ctgcccaaga atgtctagag gccacggaac ggtgccaagc acacagtccc ttttgcctct 3559

ttcacgggag caggagtccc agtgcctgtc gtggaaaggg aggaacatgc caggtccctg 3619

tgtgtccttg gccctgtctc accaaaggac tcagggctgg tttctgagtt tccgtccagt 3679

atttagccaa gttctgtgtt agtcacgtag gcctaagagc cttggcgttt acagagtcac 3739

ccagctctgg cccctggcca ttctggtcct tggcgtttac agagtcaccc agctccaggc 3799

ccctggccac tttggtactt ggttgccctt cacttcacca ggtccattcc agatgccaag 3859

agtgggcccc aggaatgtgt ttccttctct ccaccatgtt tttatagctc ttgggctggg 3919

agaagaggcg ggtctgggtc tttgtttctg agctttgttc tatgttcctc catgctacgg 3979

ttgcaattgt tttctatgaa cgagtacatt caataaagac aaccagacct gg          4031
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<210> 164

<211> 853

<212> PRT

<213> Mus musculus

<400> 164

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Glu Ser His Leu Gly Ala Leu Gly Pro Lys Asn Val Ser Gln Lys Asp
                20                  25                  30

Ala Glu Phe Glu Arg Thr Tyr Ala Asp Asp Val Asn Ser Glu Leu Val
                35                  40                  45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
        50                  55                  60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
65                  70                  75                  80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
                85                  90                  95

Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val
                100                 105                 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
                115                 120                 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
        130                 135                 140
```

Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu
145   150   155   160

Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
                165   170   175

Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys
                180   185   190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
                195   200   205

Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr
        210   215   220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225   230   235   240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
                245   250   255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp
                260   265   270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
                275   280   285

Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe
                        646/735

290   295   300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305   310   315   320

Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
                   325   330   335

Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala
                   340   345   350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser
                   355   360   365

Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser
                   370   375   380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
385   390   395   400

Arg Gln Leu Cys Ile Ala Met Asp Arg Ser Phe Asp Ala Val Gly Pro
                   405   410   415

Arg Pro Arg Leu Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
                   420   425   430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
                   435   440   445

Tyr Leu Cys Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
   450   455   460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
465   470   475   480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
          485   490   495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
          500   505   510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
          515   520   525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
          530   535   540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Tyr Ala Leu
545   550   555   560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
          565   570   575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
          580   585   590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
          595   600   605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
    610   615   620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
625   630   635   640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
         645   650   655

Val Phe Ser Val Ile His Ile Ile Ser Thr Leu Leu Leu Ser Thr Gln
         660   665   670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Phe Gly Ile Phe Arg Arg
        675   680   685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
      690   695   700

Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn
705   710   715   720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
        725   730   735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
        740   745   750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile

```
        755                 760                 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
        770             775             780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785             790             795             800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
                805             810             815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
                820             825             830

Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln Arg Asp
                835             840             845

Lys Ile Tyr Val Phe
        850
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<210> 165

<211> 3138

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84)..(2648)

<400> 165

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gccactgccg ccctgccggg gcc atg ttc gct ctg ggc ttg ccc ttc ttg gtg 113
                         Met Phe Ala Leu Gly Leu Pro Phe Leu Val
                          1   5   10

ctc ttg gtg gcc tcg gtc gag agc cat ctg ggg gtt ctg ggg ccc aag   161
Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Val Leu Gly Pro Lys
                15   20   25

aac gtc tcg cag aaa gac gcc gag ttt gag cgc acc tac gtg gac gag   209
Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu
            30   35   40

gtc aac agc gag ctg gtc aac atc tac acc ttc aac cat act gtg acc   257
Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr
            45   50   55

cgc aac agg aca gag ggc gtg cgt gtg tct gtg aac gtc ctg aac aag   305
Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys
        60   65   70

cag aag ggg gcg ccg ttg ctg ttt gtg gtc cgc cag aag gag gct gtg   353
Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
75   80   85   90

```
gtg tcc ttc cag gtg ccc cta atc ctg cga ggg atg ttt cag cgc aag      401
Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg Lys
                95                  100                 105


tac ctc tac caa aaa gtg gaa cga acc ctg tgt cag ccc ccc acc aag      449
Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys
                110                 115                 120


aat gag tcg gag att cag ttc ttc tac gtg gat gtg tcc acc ctg tca      497
Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr Leu Ser
                125                 130                 135


cca gtc aac acc aca tac cag ctc cgg gtc agc cgc atg gac gat ttt      545
Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg Met Asp Asp Phe
                140                 145                 150


gtg ctc agg act ggg gag cag ttc agc ttc aat acc aca gca gca cag      593
Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln
155                 160                 165                 170


ccc cag tac ttc aag tat gag ttc cct gaa ggc gtg gac tcg gta att      641
Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu Gly Val Asp Ser Val Ile
                175                 180                 185


gtc aag gtg acc tcc aac aag gcc ttc ccc tgc tca gtc atc tcc att      689
Val Lys Val Thr Ser Asn Lys Ala Phe Pro Cys Ser Val Ile Ser Ile
                190                 195                 200


cag gat gtg ctg tgt cct gtc tat gac ctg gac aac aac gta gcc ttc      737
Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe
```

```
    Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe
            205                 210                 215


    atc ggc atg tac cag acg atg acc aag aag gcg gcc atc acc gta cag      785
    Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln
            220                 225                 230


    cgc aaa gac ttc ccc agc aac agc ttt tat gtg gtg gtg gtg gtg aag      833
    Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val Val Lys
    235                 240                 245                 250


    acc gaa gac caa gcc tgc ggg ggc tcc ctg cct ttc tac ccc ttc gca      881
    Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala
                        255                 260                 265


    gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg      929
    Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val
                270                 275                 280


    ctg gtg tct caa gca gtc acg tct gag gca tac gtc agt ggg atg ctc      977
    Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu
            285                 290                 295


    ttt tgc ctg ggt ata ttt ctc tcc ttt tac ctg ctg acc gtc ctc ctg     1025
    Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu
            300                 305                 310


    gcc tgc tgg gag aac tgg agg cag aag aag aag acc ctg ctg gtg gcc     1073
    Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala
                            653/735
```

315   320   325   330

att gac cga gcc tgc cca gaa agc ggt cac cct cga gtc ctg gct gat   1121
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala Asp
                335   340   345

tct ttt cct ggc agt tcc cct tat gag ggt tac aac tat ggc tcc ttt   1169
Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe
                350   355   360

gag aat gtt tct gga tct acc gat ggt ctg gtt gac agc gct ggc act   1217
Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr
                365   370   375

ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag cgg cgc   1265
Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg
                380   385   390

ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc   1313
Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser
395   400   405   410

ttt gaa cct gta ggt act cgg ccc cga gtg gac tcc atg agc tct gtg   1361
Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val
                415   420   425

gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat   1409
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn
                430   435   440

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```
gtc att cgc acc aag caa tac ctc tat gtg gct gac ctg gca cgg aag          1457
Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys
        445                 450                 455


gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att          1505
Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile
        460                 465                 470


gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc          1553
Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile
475                 480                 485                 490


acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac          1601
Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr
                495                 500                 505


tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac          1649
Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn
        510                 515                 520


aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg          1697
Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu
        525                 530                 535


ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc          1745
Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg
        540                 545                 550
```

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aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt   1793
Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu
555   560   565   570

ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct   1841
Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala
             575   580   585

tgc tat cat gtg tgc ccc aac tat acc aat ttc cag ttt gac aca tcg   1889
Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser
             590   595   600

ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag   1937
Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys
             605   610   615

cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg   1985
Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu
             620   625   630

gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg   2033
Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly
635   640   645   650

aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc   2081
Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
             655   660   665

ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac   2129

Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp
        670   675   680

.

tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc   2177
Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile
        685   690   695

cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc   2225
Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val
        700   705   710

atg ggc aac gtc atc aac tgg tcg ctg gct gcc tat ggg ctt atc atg   2273
Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met
715   720   725   730

cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac   2321
Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn
            735   740   745

ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg   2369
Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly
            750   755   760

gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg   2417
Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val
            765   770   775

gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg   2465
Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp

                780   785   790

cag aaa acc cct gca gag tcg agg gag cac aac cgg gac tgc atc ctc   2513
Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu
795   800   805   810

ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc   2561
Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile
                   815   820   825

gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg   2609
Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly
                   830   835   840

tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg   2658
Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly
                   845   850   855

tccacacccc aggtgttgct gacactggat gacgacctgg atacttagaa aggggcttca 2718

ggaagggatg tgctgtttcc ctctacgtgc ccagtcctag cctcgctcta ggacccaggg 2778

ctggcttcta agtttccgtc cagtcttcag gcaagttctg tgttagtcat gcacacacat 2838

acctatgaaa ccttggagtt tacaaagaat tgccccagct ctgggcaccc tggccaccct 2898

ggtccttgga tccccttcgt cccacctggt ccaccccaga tgctgaggat gggggagctc 2958

aggcgggggcc tctgctttgg ggatgggaat gtgttttct cccaaacttg tttttatagc 3018

tctgcttgaa gggctgggag atgaggtggg tctggatctt ttctcagagc gtctccatgc 3078

tatggttgca tttccgtttt ctatgaatga atttgcattc aataaacaac cagactcagt 3138

<210> 166

<211> 855

<212> PRT

<213> Homo sapiens

<400> 166

Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser Val
1   5   10   15

Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln Lys Asp
                20   25   30

Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser Glu Leu Val
                35   40   45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
        50   55   60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
65   70   75   80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
                85   90   95

Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val
            100   105   110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
            115   120   125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
            130   135   140

Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu
145   150   155   160

Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
                    165   170   175

Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn
                    180   185   190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
                    195   200   205

Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr
            210   215   220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225   230   235   240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
                              660/735

                    245   250   255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp
            260   265   270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
            275   280   285

Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe
            290   295   300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305   310   315   320

Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
                325   330   335

Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser
            340   345   350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser
            355   360   365

Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly
            370   375   380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
385   390   395   400

Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr
          405   410   415

Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
          420   425   430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
          435   440   445

Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
          450   455   460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
465   470   475   480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
          485   490   495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
          500   505   510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
          515   520   525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
          530   535   540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu
545   550   555   560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
          565   570   575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
          580   585   590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
          595   600   605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
          610   615   620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
625   630   635   640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
          645   650   655

Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln
          660   665   670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg
          675   680   685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
          690   695   700

Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn
                    663/735

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        705                     710                     715                     720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
                    725                     730                     735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
                    740                     745                     750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
                    755                     760                     765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
                    770                     775                     780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785                     790                     795                     800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
                    805                     810                     815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
                    820                     825                     830

Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser
                    835                     840                     845

Ser Cys Leu Leu Pro Cys Gly
850                     855
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<210> 167

<211> 2815

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56)..(571)

<400> 167

gcgaagcgcg cctgcgaccc ggcgtccggg cgcgctggag aggacgcgag gagcc atg   58
                                                                    Met
                                                                     1

agg cgc cag cct gcg aag gtg gcg gcg ctg ctg ctc ggg ctg ctc ttg   106
Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu
             5   10   15

gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat   154
Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr
        20   25   30

cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg   202
Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg
        35   40   45

tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc   250

```
Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe
50              55              60              65


ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc   298
Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile
                70              75              80


cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat   346
Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn
                85              90              95


gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag   394
Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln
        100             105             110


ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct   442
Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro
        115             120             125


gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc   490
Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro
130             135             140             145


cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct   538
Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro
            150             155             160


ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca 591
Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
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165   170

agaggaggga caggagaggg cctttccctg gcctttctgt cttcgttgat gttcacttcc 651

aggaacggtc tcgtgggctg ctaagggcag ttcctctgat atcctcacag caagcacagc 711

tctctttcag gctttccatg gagtacaata tatgaactca cactttgtct cctctgttgc 771

ttctgtttct gacgcagtct gtgctctcac atggtagtgt ggtgacagtc cccgagggct 831

gacgtcctta cggtggcgtg accagatcta cgggagagag actgagagga agaaggcagt 891

gctggaggtg caggtggcat gtagaggggc caggccgagc atcccaggca agcatccttc 951

tgcccgggta ttaataggaa gccccatgcc gggcggctca gccgatgaag cagcagccga 1011

ctgagctgag cccagcaggt catctgctcc agcctgtcct ctcgtcagcc ttcctcttcc 1071

agaagctgtt ggagagacat tcaggagaga gcaagcccct tgtcatgttt ctgtctctgt 1131

tcatatccta aagatagact tctcctgcac cgccagggaa gggtagcacg tgcagctctc 1191

accgcaggat ggggcctaga atcaggcttg ccttggaggc ctgacagtga tctgacatcc 1251

actaagcaaa tttatttaaa ttcatgggaa atcacttcct gccccaaact gagacattgc 1311

attttgtgag ctcttggtct gatttggaga aaggactgtt acccattttt ttggtgtgtt 1371

tatggaagtg catgtagagc gtcctgccct ttgaaatcag actgggtgtg tgtcttccct 1431

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gacaactgcg tgggtccaaa cactcctctt cctccaggtc atttgttttg cattttttaat 2331

gtctttattt tttgtaatga aaaagcacac taagctgccc ctggaatcgg gtgcagctga 2391

ataggcaccc aaaagtccgt gactaaattt cgtttgtctt tttgatagca aattatgtta 2451

agagacagtg atggctaggg ctcaacaatt ttgtattccc atgtttgtgt gagacagagt 2511

ttgtttttccc ttgaacttgg ttagaattgt gctactgtga acgctgatcc tgcatatgga 2571

agttccgctt cggtgacatt tcctggccat tcttgtttcc attgtgtgga tggtgggttg 2631

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cagagtaaac ttgaagcaga tctgtgcatg cttttcctct gcaacaattg gctcgtttct 2751

cttttttgtt ctcttttgat aggatcctgt ttcctatgtg tgcaaaataa aaataaattt 2811

gggc 2815

<210> 168

<211> 172

<212> PRT

<213> Homo sapiens

<400> 168

Met Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu
1   5   10   15

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Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu
            20   25   30

Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser
            35   40   45

Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp
            50   55   60

Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe
65   70   75   80

Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
                    85   90   95

Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln
            100   105   110

Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn
            115   120   125

Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser
            130   135   140

Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Ala Tyr Cys Asn Thr
145   150   155   160

Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys

670/735

<210> 169

<211> 3337

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136).. (1755)

<400> 169

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tacccgagtc tcgtttcctc tcagtccatc caccttcat ggggccagag ccctctctcc 120

agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171
                Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile
                 1   5   10

tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219
Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu
         15   20   25

cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267
Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala
     30   35   40

acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat   315
Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn
45   50   55   60

acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg   363
Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu
               65   70   75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac   411
Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr
               80   85   90

cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag   459
Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu
               95   100   105

cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg   507
Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala
   110   115   120

gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac   555
Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr
125   130   135   140

ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat   603
Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn
              145   150   155

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tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat    651
Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn
            160             165             170


cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc    699
Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser
            175             180             185


cct ctg acc tcc agc ggg cat cag gag cag gac aca gaa ctg ggc agt    747
Pro Leu Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser
            190             195             200


acc cac aca gca ggt gcg acc tcc agc ctc aca cca tcc cgt ggg cct    795
Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro
205             210             215             220


gtg tct cca tct gtc tcc ttc cag ccc ctg gcc cgt tcc acc ccc agg    843
Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg
            225             230             235


gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc    891
Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr
            240             245             250


tcc ttc tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag    939
Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu
            255             260             265


ggt aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc    987
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Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser
        270   275   280

agt ggg gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc   1035
Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr
285   290   295   300

acc ttg atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca   1083
Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro
                    305   310   315

gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc   1131
Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro
                    320   325   330

cct ggt gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa   1179
Pro Gly Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys
            335   340   345

ttg ccc atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct   1227
Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro
        350   355   360

act agc atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac   1275
Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp
365   370   375   380

ggg agc agc aga aat gag gag acc cca gca gct cca aca ccc gcc ggc   1323
Gly Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly
                            674/735

385   390   395

gcc act gga ggc agc tca gcc tgg cta gac agc agc tct gag aat agg   1371
Ala Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg
         400   405   410

ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta   1419
Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val
         415   420   425

gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc   1467
Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser
         430   435   440

acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat   1515
Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr
445   450   455   460

aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc   1563
Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile
         465   470   475

cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc   1611
Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly
         480   485   490

ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc   1659
Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys
         495   500   505

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cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggg     1707
His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly
        510                 515                 520


gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac     1755
Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
525                 530                 535                 540
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tagtgaagcc ctgggctctt cccaccaccc atctgttccg ttcctgcagt atacctggcc 1815

cctctccgaa gcccctcttt ccctcccctc tggtctccat tctcttcagc tccctacatg 1875

ggctgggggag gagacacctg gtgggcagag ctcaggcaga ggtttggatt tcagctccct 1935

cacttccggg gctgtgtggc tttggcagat gtcagacttc tggtcttgct tctccacgtg 1995

gacagtgagt atctggctca ttcttcactg ggttcttctg agattgaacc tacaggtgtt 2055

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cacaggcagc ctaggcctgc gtcccaacct gcctctcacc agctctgtga ccttgggcaa 2235

gggatttatc tgtctgtccc ttagttttct cacctgtaaa aggaggataa gtatatatat 2295

atatttccca gtgttgtgaa gattaaagga gtttatcgat gtaggtctta ggatgagtcc 2355

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tggcatttac caagggttgg atatatgtta ttatcactat taagtgttga gggtccaggc 2415


atgctgggca acagggaccc catctctaca aaaaagttta aaaaattagc caggcgtggt 2475


ggtgcacctg tcgtcttagc tacttgggag gctgaggtgg gaggatcgct tgagcccgga 2535


agcttgaagc tgcagtgagc taggatcgtg ccactgcact ccaacctggg tgagagagcg 2595


agaccctgtc tcaagaaaaa gaaaaatgca gagaaacagg agtcttggct actcctttag 2655


aggcagactc agaccctcct gcctcacagc tttatctttg tatttgcccc ttactttatc 2715


ttgtgccttg agaaattgct ggggagagag gtatgtccac tgggcagctg tacaggatgg 2775


aggatatagg gcgtttccac tcccagcagc caggttccct caccccaagc tcacccactg 2835


ttggggagat tatctacaat aacaccagaa acacattggg gtggattggg ggtatcctta 2895


tgggttcttt tcagggaacc attgctggac aaggcacagg agccacctcc atttctgagc 2955


tctgcaaggg acaagaacta gagccatcag gggctgggct cactgtggcc ccaccccaag 3015


ccgtcagcct ccagggatct acaccctgcc ttggctgcta cagctttttc actccactgc 3075


cctaggggag ttcagcaacc taatgatctc tatctctgaa catctcttca tcccatgctc 3135


caagtccagc aacctgcacc ctggaaccag gagtggaccc tacccgggct gtctgtatta 3195


atccccatcc cccaccacca atcttaaaaa gccctctgtc cccctaccct aaaccccagt 3255
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ttaccgttcc agggtagctt tg   3337

<210> 170

<211> 540

<212> PRT

<213> Homo sapiens

<400> 170

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe
1   5   10   15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
                20   25   30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
            35   40   45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg
        50   55   60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu
65   70   75   80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln
                85   90   95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu
          100   105   110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile
          115   120   125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
          130   135   140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145   150   155   160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
              165   170   175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
          180   185   190

Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala
          195   200   205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
          210   215   220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
225   230   235   240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser

```
                    245                 250                 255

Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly
            260                 265                 270


Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu
            275                 280                 285


Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
            290                 295                 300


Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
305                 310                 315                 320


Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
                325                 330                 335


Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn
            340                 345                 350


Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val
            355                 360                 365


Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg
            370                 375                 380


Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
385                 390                 395                 400
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Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser
              405               410               415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
              420               425               430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
              435               440               445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
              450               455               460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465               470               475               480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
              485               490               495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
              500               505               510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
              515               520               525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
              530               535               540
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681/735

<210> 171

<211> 3579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (242)..(3094)

<400> 171

gtagtttcgg ctcggcagac ccggcgagcc cagtggccgc gctccggtgc ggcggcgccc 60

gaggcccgag gcggaagtgg gacggccaag cagggaagcg agggctcggg atcgacggcc 120

gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccg 180

gggaaggagg cagggcaagg ccgggcttgg gggcaggtgg tccgggcatc cagccttgaa 240

g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289
  Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala
  1   5   10   15

gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg   337
Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu
            20   25   30

atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc   385
Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe
            35   40   45

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ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc      433
Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
     50                  55                  60


aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc      481
Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
 65                  70                  75                  80


atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac      529
Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
                 85                  90                  95


ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga      577
Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
                100                 105                 110


gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag      625
Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
            115                 120                 125


cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg      673
Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
        130                 135                 140


gcg ctc tat cag aca gca att gaa agc gcc aga caa gct gga gac agc      721
Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
145                 150                 155                 160
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gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg   769
Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
                 165   170   175

ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg   817
Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
                 180   185   190

ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc   865
Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
                 195   200   205

cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc   913
Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro
                 210   215   220

agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca   961
Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro
225   230   235   240

ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct   1009
Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro
                 245   250   255

ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc   1057
Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu
                 260   265   270

cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc   1105

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg
     275   280   285

gtg gct aag agc ttt gat gct gtc ttg gag gcc ctg agc cgg ggt gag   1153
Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu
     290   295   300

ccc gtg gac ctc tcc tgc ctg ccc cct cca ccc gac cag ctg ccc cca   1201
Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro
305   310   315   320

gac cca ccg tca cca ccg tcg cag cct ccg acc ccc gct acg gcg ccc   1249
Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
           325   330   335

tcc aca aca gag gtg ccc cca ccc ccg agg acc ctg ctg gag gcg ctg   1297
Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
          340   345   350

gag cag cgg atg gag cgg tac cag gtg gcc gca gcc cag gcc aag agc   1345
Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser
        355   360   365

aag ggg gac cag cgg aaa gct cga atg cac gag cgc atc gtc aag caa   1393
Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
       370   375   380

tac caa gat gcc atc cga gcc cac aag gct ggc cga gcc gtg gat gtc   1441
Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val

385   390   395   400

gct gaa ttg ccc gtg ccc cca ggc ttc ccc cca atc cag ggc ctg gag 1489
Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
      405   410   415

gcc acc aag ccc acc cag cag agt ctg gtg ggt gtc ctg gag act gcc 1537
Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
      420   425   430

atg aag ctg gcc aac cag gat gaa ggc cca gag gat gaa gag gat gag 1585
Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
     435   440   445

gtg cct aag aag cag aac agc cct gtg gcc ccc aca gcc cag ccc aaa 1633
Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
     450   455   460

gcc cca ccc tca aga act ccc cag tcg gga tca gcc cca aca gcc aaa 1681
Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
465   470   475   480

gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc 1729
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
     485   490   495

cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag 1777
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
     500   505   510

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cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag     1825
Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys
        515                 520                 525


gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac     1873
Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp
        530                 535                 540


atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg     1921
Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu
545                 550                 555                 560


gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat     1969
Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
                565                 570                 575


ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac     2017
Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
        580                 585                 590


cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag     2065
His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys
        595                 600                 605


ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag     2113
Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys
        610                 615                 620
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caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa   2161
Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
625   630   635   640

agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac   2209
Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
            645   650   655

atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga   2257
Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
            660   665   670

ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat   2305
Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
            675   680   685

ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac   2353
Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
            690   695   700

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc   2401
Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705   710   715   720

agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc   2449
Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
            725   730   735

gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg   2497
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    Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
                    740                 745             750


    aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg    2545
    Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
                755                 760             765


    gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg    2593
    Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
                770                 775             780


    gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag    2641
    Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
    785                 790                 795                 800


    acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg    2689
    Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
                    805                 810                 815


    ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc    2737
    Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
                    820                 825                 830


    cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc    2785
    Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
                835                 840             845


    agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc    2833
    Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala
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            850                855                860

ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac      2881
Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr
865                870                875                880


cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag      2929
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln
                    885                890                895


ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag      2977
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln
                900                905                910


ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc      3025
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser
            915                920                925


agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt      3073
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser
            930                935                940


gag ctg cag cgg ctc cgc agg tgaggagccc atggggcggg cagcccccag        3124
Glu Leu Gln Arg Leu Arg Arg
945                950


aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca   3184


gacaatcagc ggacaatcgg ttctggactc accccctcatc cgggcccccca gccccgccag  3244
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agcctccgtg gctgcgggtg ttgggaacca tgcctgccag ccagtatgtg cccctcaccc 3304

aggcctggct gggccctgga gagtcctgtt tgcacagccc aggggtgtcc ggcctctggc 3364

ccgccccgga gcagggaggg cggctggggc caagccccga gggcccctgc aagcacttta 3424

cttcctgttc ctccccagcc ttaaccccaa agccctcctg caccccaaag aagccactga 3484

ggctggccga gccacactgt ctccccaggg gcgtcgacct ggcccagctg ggtccccagg 3544

ccagcacatg gaataaaata gccagggcca cactc   3579

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<210> 172

<211> 951

<212> PRT

<213> Homo sapiens

<400> 172

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1   5   10   15

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

                 20   25   30

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

                 35   40   45

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
    50   55   60

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
    65   70   75   80

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
          85   90   95

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
        100   105   110

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
        115   120   125

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
        130   135   140

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
145   150   155   160

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
        165   170   175

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
        180   185   190

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
        195   200   205

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Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro
     210   215   220

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro
225   230   235   240

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro
           245   250   255

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu
           260   265   270

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg
           275   280   285

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu
     290   295   300

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Asp Gln Leu Pro Pro
305   310   315   320

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
           325   330   335

Ser Thr Thr Glu Val Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
           340   345   350

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser

                    355   360   365

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
        370   375   380

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val
385   390   395   400

Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
                    405   410   415

Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
                        420   425   430

Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
                    435   440   445

Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
        450   455   460

Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
465   470   475   480

Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
                    485   490   495

Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
                    500   505   510

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys
        515   520   525

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp
        530   535   540

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu
545   550   555   560

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
                565   570   575

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
                580   585   590

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys
        595   600   605

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys
        610   615   620

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
625   630   635   640

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
                645   650   655

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
                660   665   670

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Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
        675   680   685

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
        690   695   700

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705   710   715   720

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
                725   730   735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
                740   745   750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
                755   760   765

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
        770   775   780

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
785   790   795   800

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
                805   810   815

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala

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                820                   825                   830


Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
        835                   840                   845


Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala
        850                   855                   860


Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr
865                   870                   875                   880


Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln
                885                   890                   895


Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln
                900                   905                   910


Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser
        915                   920                   925


Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser
        930                   935                   940


Glu Leu Gln Arg Leu Arg Arg
945                   950
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<210> 173

<211> 2796

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (574)..(1683)

<400> 173

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tagtccttaa caaagggaaa gcgataaatg taaataagct cacattttca gaatgagcgg 180

tttgcagtaa ggagctgcgg cagcccagag tctgctcttt ttgggctggg ctaacctttc 240

cctgtttttt gtttttttgtt ttgttttgtt tttgttttttt atggataaaa atatgcgctt 300

ccgaagtgcg agttgccagt ttacacgttt attagctaac tatctacagg catgagcaca 360

ttctctcatc tagcacactc tttcttgggc actcaattga ggaactctct gatcgtctgc 420

ctccagaaaa ttcattgatt atccaagtct cagataaatc tggtgccaga gtttggtttg 480

aactaactaa tgaagaaagc attctctact ggtcctcagt ctcaagagtg gtgaacccct 540

gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594
                                    Met Gly Asp Arg Arg Phe Ile

```
                                      1                5


gac ttc caa ttc caa gat tta aat tca agt ctc aga ccc agg ttg gga   642
Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly
            10                  15                  20


aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat   690
Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr
            25                  30                  35


aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata   738
Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile
    40                  45                  50                  55


acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga   786
Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg
                    60                  65                  70


agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt   834
Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu
                75                  80                  85


ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac   882
Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His
            90                  95                  100


tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc   930
Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu
    105                 110                 115
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acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat   978
Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp
120   125   130   135

cgt ttc cta gcc att gtc tat ccc ttc cga tcg cgt acc atc agg acc   1026
Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr
              140   145   150

agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc   1074
Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu
              155   160   165

agt ggt ggt att tca gct tct ttg ttc tcc acc act aat gtc aac aat   1122
Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn
              170   175   180

gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca   1170
Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr
185   190   195

tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att   1218
Tyr Leu Ser Lys Ile Thr Ile Phe Ile Glu Val Val Gly Phe Ile Ile
200   205   210   215

cct ctg ata ttg aat gtt tct tgt tct tct gtg gtg ctt aga acc ctc   1266
Pro Leu Ile Leu Asn Val Ser Cys Ser Ser Val Val Leu Arg Thr Leu
              220   225   230

cgc aag cct gca aca ttg tct cag att ggg acc aat aag aaa aaa gtg   1314
Arg Lys Pro Ala Thr Leu Ser Gln Ile Gly Thr Asn Lys Lys Lys Val
         235   240   245

ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta   1362
Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val
         250   255   260

cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc   1410
Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala
         265   270   275

att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att   1458
Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile
280   285   290   295

acc ttg tgc ctt gca act ctg aat tgt tgc ttt gat cct ttt atc tat   1506
Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr
         300   305   310

tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat   1554
Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His
         315   320   325

ata agg atg gag tcg ctg ttt aag act gag aca cct ctg acc ccc aaa   1602
Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys
         330   335   340

cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat   1650

Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn
          345   350   355

aat ggt ggt gaa tta atg ctg gaa tcc acc ttc taggtaccag aattgtcttt 1703
Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe
     360   365   370

caggttcagc tacagtgtct cttatgattt ttttcctatg ctataaatag gagaaacaaa 1763

ttgaagctaa tgatactgag aatagagtaa tgtaccaaat gcagtcagat acatttgttt 1823

gaacactatt gtacatattc tgttttgttc agtaattata ggtcaagtct aattacaaca 1883

accaaaacag atcagcctct tctgttgagt tgacttttca ttacctaaat gaccagtggt 1943

cttgactttt agtgatgtga gggttatttt taaacttaaa aaaaaggca ttccagtaat 2003

tttggtaatt gggttgggcc tataaatata gaacaaattc agggattatt taaaaacatc 2063

tgtgttacta ctgatatatg ctagtatttt tttccttttt tgaattaata ttgaatttat 2123

tttaaaaaaa gaactatttt tacctaatct taataagaca tactgagaaa gagaaatgtg 2183

ttgaatttta aaatattggc aaattttacc tagattttaa aaacctaaat gaagtgtttg 2243

aatgaatatg ggtgggaaat ttggaattta gacaacattt acgcatttat aataaccaca 2303

attagtgtca gcttttaaaa ctttcttttt aaaataattc tagaattttc atatgaaatt 2363

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gttaatcctg aaaggtgcta cttatgtgcc tggcaggtat aaaatggaaa actcataaaa 2423

ttaacagtgt caatttaaaa aaaaaaaaac tttaagcaac actatattat ttcttaagat 2483

tttcatttat cctttatggg ggtggggatt ggcttgtaga aaatatttat tcttcatgtt 2543

aaatgttggg gacacattac agccagagag ctacagtatt tgtgcccagg tcaggagtaa 2603

attgaaaaag taagtgaata gaatagtagc agcaagatat cttagagctt atattagtag 2663

tttttaaggt ggtggttaga tagctgtaat tttgaaatcc atactctctt ctgtacattt 2723

tggagcacat tgtagccaag gcgctgctga atttgtgctc aggtcgggag catattgaaa 2783

aagatgtgta cat   2796

<210> 174

<211> 370

<212> PRT

<213> Mus musculus

<400> 174

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Leu Asn Ser
1   5   10   15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
                20   25   30

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Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
     35   40   45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe
    50   55   60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn
    65   70   75   80

Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
            85   90   95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
          100   105   110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
         115   120   125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
       130   135   140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
145   150   155   160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
         165   170   175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
         180   185   190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
    195   200   205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
    210   215   220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225   230   235   240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
          245   250   255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
          260   265   270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe
      275   280   285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
    290   295   300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305   310   315   320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr
          325   330   335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu

340   345   350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser

    355   360   365

Thr Phe

  370

<210> 175

<211> 2299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)..(1176)

<400> 175

cctaccggtc catagtgtca gagtggtgaa cccctgcagc cagcaggcct cctgaaaaaa 60

aagtcc atg ggt gac aga aga ttc att gac ttc caa ttc caa gat tca 108

   Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser

    1   5   10

aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act 156

Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr

15   20   25   30

```
tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac      204
Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr
            35                  40                  45
```

```
agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt      252
Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe
            50                  55                  60
```

```
gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc      300
Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile
            65                  70                  75
```

```
acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt      348
Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe
            80                  85                  90
```

```
aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc      396
Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu
95                  100                 105                 110
```

```
tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg      444
Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met
            115                 120                 125
```

```
ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat      492
Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr
            130                 135                 140
```

```
cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg      540
Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val
        145                 150                 155


tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct      588
Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser
        160                 165                 170


ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa      636
Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu
175                 180                 185                 190


ggc ttc tcc aaa cgt gtc tgg aag act tat tta tcc aag atc aca ata      684
Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile
                195                 200                 205


ttt att gaa gtt gtt ggg ttt atc att cct cta ata ttg aat gtc tct      732
Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser
                210                 215                 220


tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct      780
Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser
        225                 230                 235


caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat      828
Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His
        240                 245                 250


atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc      876
```

```
Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe
255             260             265                 270


ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa    924
Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu
                275             280             285


aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg    972
Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu
                290             295             300


aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt   1020
Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe
                305             310             315


cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt   1068
Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe
                320             325             330


aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa   1116
Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln
335             340             345                 350


gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta   1164
Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu
                355             360             365


gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc       1216
Glu Ser Thr Phe
```

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370

ctataatttt tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc 1276

accaaatcca gtcagataca tttgtttgaa ggtatactgt agagttttta ttgctgtttt 1336

gttcagtaat tataggtcaa atctaattac aacaaccaag atggattgcc aaactcttct 1396

gcttggttgg aatttcattg tatcgcatta tccaggtggc tagtggcatt tgataatata 1456

gagatgactt tgaaactttc aaaaaggtat ttctattcca atgatatttg gtaattaggt 1516

tgggcctata aatatagaac aaattcaggg attttaaaa aattgtgtta ctactgatat 1576

atgctagttt tattttattt ttttggactg tcattgagtt tattttagca caagaatatt 1636

tttagcctaa cattattaat aagaaatgtg tcaaattttt aacattggta aaatatgtta 1696

tgtgcatttt gaaaacagaa aacaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756

aaaattaaca ggatttacac aattataatc accagcagtg tgagtttaaa aaacttcgtt 1816

gttttacac caaattaaaa ttttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876

gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936

tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056

ctgcatttgt gcccaggtca ggagcaaatt gaaaaaaaaa ataaagtaat actaaaaaat 2116

caaactataa acccaaaaca tttattaaaa cctgaattaa tcctttttgg agggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236

caggagctgc tgaatttgtg cccctggatt ggaaccaaat aaaaaaaaaa aaaaaaaatt 2296

cct   2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser
1   5   10   15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
            20   25   30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
            35   40   45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe
            50   55   60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn
65   70   75   80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
                    85   90   95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
                    100   105   110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
                    115   120   125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
                    130   135   140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
145   150   155   160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
                    165   170   175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
                    180   185   190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
                    195   200   205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
                    712/735

                  210   215   220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225   230   235   240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
                       245   250   255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
                       260   265   270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe
                       275   280   285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
                       290   295   300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305   310   315   320

Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr
                       325   330   335

Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
                       340   345   350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
                       355   360   365

Thr Phe
370

<210> 177

<211> 973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (30)..(416)

<400> 177

cagacagcgg cgggcgcagg acgtgcact atg gct cgg ggc tcg ctg cgc cgg   53
                                  Met Ala Arg Gly Ser Leu Arg Arg
                                   1   5

ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc   101
Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
     10   15   20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc   149
Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
 25   30   35   40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg   197
Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg

```
                45                      50                      55


gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct    245
Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
             60                      65                      70


gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg    293
Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
             75                      80                      85


acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc    341
Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
             90                      95                      100


cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag    389
Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
105                 110                 115                 120


ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccccctgcca    436
Gly Cys Pro Ala Val Ala Leu Ile Gln
                125


gccggggctc gcccactcat cattcattca tccattctag agccagtctc tgcctcccag 496


acgcggcggg agccaagctc ctccaaccac aagggggggtg ggggggcggtg aatcacctcc 556


gaggcctggg tccagggttc aggggaacct tccaaggtgt ctggttgccc tgcctctggc 616


tccagaacag aaagggagcc tcacgctggc tcacacaaaa cagctgacac tgactaagga 676
```

actgcagcat ttgcacaggg gagggggtg ccctccttcc tagaggccct gggggccagg 736

ctgacttggg gggcagactt gacactaggc cccactcact cagatgtcct gaaattccac 796

cacgggggtc accctggggg gttagggacc tatttttaac actaggggc tggcccacta 856

ggagggctgg ccctaagata cagacccccc caactcccca aagcggggag gagatattta 916

ttttggggag agtttggagg ggaggggagaa tttattaata aaagaatctt taacttt   973

<210> 178

<211> 129

<212> PRT

<213> Homo sapiens

<400> 178

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Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
 1               5                  10                  15

Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
            20                  25                  30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
        35                  40                  45

Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
    50                  55                  60
```

Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro

65   70   75   80

Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser

        85   90   95

Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr

        100   105   110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile

        115   120   125

Gln

<210> 179

<211> 3631

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (191)..(3244)

<400> 179

tctaaatcag cggccgctga attctagggc gctgctggcg ctgcagctgc acttgctccg 60

ggcgctggcg caagatgatg ttgctccata ttttaaaacg gagccaggcc taccacagat 120

ccacctggaa gggaaccgcc ttgttctcac ctgccttgcc gaagggagct ggcctttgga 180

gttcaagtgg atg cgc gat gac agt gag ctc acc acc tac agc agc gaa 229
     Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu
     1   5   10

tat aag tac att att cca tct ttg cag aag ctc gat gct ggg ttt tac 277
Tyr Lys Tyr Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr
  15   20   25

cgc tgc gtg gtg cga aac aga atg gga gca ctc ctg caa aga aaa tca 325
Arg Cys Val Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser
30   35   40   45

gaa gtt caa gtc gca tat atg gga agt ttc atg gat acg gac cag agg 373
Glu Val Gln Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg
    50   55   60

aaa aca gtt tct caa gga cgt gca gcg att cta aac ctg ctg ccc atc 421
Lys Thr Val Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile
    65   70   75

acc agc tac ccc aga cct caa gtg act tgg ttt aga gaa ggg cac aag 469
Thr Ser Tyr Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys
    80   85   90

att att cca agc aac aga ata gcc atc aca ttg gag aat cag ctg gtg 517

Ile Ile Pro Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val
    95   100   105

atc ctc gcc acc aca acc agt gat gcc ggg gca tac tac gtg cag gcc   565
Ile Leu Ala Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala
110   115   120   125

gtg aat gag aaa aat gga gaa aac aag aca agc cca ttc att cat ttg   613
Val Asn Glu Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu
              130   135   140

agc ata gca aga gat gtt ggc aca cct gaa acc atg gcc cca acc att   661
Ser Ile Ala Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile
              145   150   155

gtg gtt ccc ccg ggc aac aga agt gtg gtg gct gga tcc agt gag acc   709
Val Val Pro Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr
              160   165   170

acc ttg gaa tgt ata gcc agt gcc agg cct gtg gag gac ctg agt gtg   757
Thr Leu Glu Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val
        175   180   185

acc tgg aag agg aat gga gtg aga atc acc agt ggc ctc cac agc ttt   805
Thr Trp Lys Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe
190   195   200   205

gga aga cgc ctc acc atc agc aac ccg acg tcc gcg gac acc ggg cca   853
Gly Arg Arg Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro

```
                210                  215                  220


tac gtc tgc gag gcg gcg ctg ccg ggg agc gct ttt gaa ccg gcc agg    901
Tyr Val Cys Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg
            225                  230                  235


gcg acg gcc ttt ctt ttc atc ata gag cca cca tat ttt act gct gag    949
Ala Thr Ala Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu
            240                  245                  250


ccc gag agt cgg att tca gct gaa gta gaa gaa act gtg gac atc gga    997
Pro Glu Ser Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly
            255                  260                  265


tgt caa gcc atg ggg gtc ccc ctt ccc acc ctc cag tgg tac aag gat   1045
Cys Gln Ala Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp
270                  275                  280                  285


gcc atc tcc atc agc agg ctc cag aat cct cga tac aaa gtg ctc gcc   1093
Ala Ile Ser Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala
            290                  295                  300


agc gga ggc ctg cgc atc cag aag ctg cgt cca gag gac tcc gga atc   1141
Ser Gly Gly Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile
            305                  310                  315


ttc cag tgc ttc gcc agc aat gaa gga ggg gag atc cag acc cac acc   1189
Phe Gln Cys Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr
            320                  325                  330
```

```
tac ctg gat gta acc aat atc gct cca gtg ttc acc cag cgg cca gtg    1237
Tyr Leu Asp Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val
    335             340             345


gac acc aca gtt act gac ggg atg aca gcc att cta agg tgt gag gtg    1285
Asp Thr Thr Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val
350             355             360             365


tcc ggg gct ccc aaa ccc gcc atc acc tgg aaa aga gaa aac cac att    1333
Ser Gly Ala Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile
                370             375             380


ctg gcc agt ggc tct gtc cgg att cct agg ttc atg ctt ctt gaa tcg    1381
Leu Ala Ser Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser
                385             390             395


ggg ggt cta cag atc gcg ccc gtc ttc atc cag gat gcc ggc aac tac    1429
Gly Gly Leu Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr
            400             405             410


acc tgc tat gcg gcc aac aca gag ggc tcc ctg aat gca tcg gcc acg    1477
Thr Cys Tyr Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr
            415             420             425


ctc act gtg tgg aat cgg acg tcc atc gtc cac cct cct gag gac cac    1525
Leu Thr Val Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His
430             435             440             445
```

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```
gtg gtg att aag ggg acc acg gcc acg ctg cac tgt ggt gcc aca cat     1573
Val Val Ile Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His
            450                 455                 460


gac ccc cgg gtt tca ctc cgc tac gtt tgg aag aag gac aac gtg gcc     1621
Asp Pro Arg Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala
            465                 470                 475


ctg act cca tcg agc acg tct agg atc gtg gtg gag aag gac ggg tcc     1669
Leu Thr Pro Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser
            480                 485                 490


ctt ctc atc agc cag acg tgg tca ggc gac atc ggt gac tac agc tgc     1717
Leu Leu Ile Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys
            495                 500                 505


gag att gtt tct gaa gga ggg aat gac tcc agg atg gcc cgg ctg gaa     1765
Glu Ile Val Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu
510                 515                 520                 525


gtg att gaa ctg cct cat tca cct cag aac ctc ctg gtc agc cct aat     1813
Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn
            530                 535                 540


tct tcc cac agc cac gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat     1861
Ser Ser His Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp
            545                 550                 555


gga aac agt cct att ctt tat tac atc gtg gag ctg tct gaa aac aac     1909
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        Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn
                    560                 565                 570


        tct cca tgg aag gtg cat ctg tca aac gtt ggc cct gag atg aca ggc      1957
        Ser Pro Trp Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly
            575                 580                 585


        gtc acc gtg agt ggc ctg act ccg gct cgt acc tat caa ttc cgg gtg      2005
        Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val
        590                 595                 600                 605


        tgc gcg gtg aat gaa gtg ggc agg ggc cag tac agt gcc gag aca agc      2053
        Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser
                    610                 615                 620


        agg ttg atg cta cct gaa gaa cca ccc agt gct ccc ccg aaa aat ata      2101
        Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile
                    625                 630                 635


        gtg gcc agt ggg cgg act aat cag tcc att atg gtc cag tgg cag cca      2149
        Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro
                    640                 645                 650


        ccc cca gaa aca gag cac aac ggg gtg ttg cgt gga tac atc ctc agg      2197
        Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg
            655                 660                 665


        tac cgc ctg gct ggc ctt ccc gga gag tac cag cag cgg aac atc acc      2245
        Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr
```

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                670                   675                   680                   685


agc ccg gag gtg aac tac tgc ctg gtg aca gac ctg atc atc tgg aca    2293
Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr
                          690                   695                   700


cag tat gag ata cag gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc    2341
Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val
                          705                   710                   715


ttc agc agg gca gtg acc gag tac acc ttg cag gga gtg ccc acc gcg    2389
Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala
                          720                   725                   730


ccc ccg cag aac gtg cag acg gaa gcc gtg aac tcc acc acc att cag    2437
Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln
                          735                   740                   745


ttc ctg tgg aac cct ccg cct cag cag ttt atc aat ggc atc aac cag    2485
Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln
750                   755                   760                   765


gga tac aag ctt ctg gca tgg ccg gca gat gcc ccc gag gct gtc act    2533
Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr
                          770                   775                   780


gtg gtc act att gcc cca gat ttc cac gga gtc cac cat gga cac ata    2581
Val Val Thr Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile
                          785                   790                   795
```

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acg aac ctg aag aag ttt acc gcc tac ttc act tcc gtt ctg tgc ttc    2629
Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe
        800             805             810


acc acc cct ggg gac ggg cct ccc agc aca cct cag ctg gtc tgg act    2677
Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr
        815             820             825


cag gaa gac aaa cca gga gct gtg gga cat ctg agt ttc aca gag atc    2725
Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile
830             835             840             845


ttg gac aca tct ctc aag gtc agc tgg cag gag ccc ctg gag aaa aat    2773
Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn
            850             855             860


ggc atc att act ggc tat cag atc tct tgg gaa gtg tac ggc agg aac    2821
Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn
            865             870             875


gac tct cgt ctc acg cac acc ctg aac agc acg acg cac gag tac aag    2869
Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys
        880             885             890


atc caa ggc ctc tca tct ctc acc acc tac acc atc gac gtg gcc gct    2917
Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala
        895             900             905
```

```
gtg act gcc gtg ggc act ggc ctg gtg act tca tcc acc att tct tct    2965
Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser
910                 915                 920                 925


gga gtg ccc cca gac ctt cct ggt gcc cca tcc aac ctg gtc att tcc    3013
Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser
                    930                 935                 940


aac atc agc cct cgc tcc gcc acc ctt cag ttc cgg cca ggc tat gac    3061
Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp
                    945                 950                 955


ggg aaa acg tcc atc tcc agg tgg att gtt gag ggg cag atg aga cat    3109
Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His
                960                 965                 970


caa ggt gtt gga tta cct gcc gag gtc aca cag cca agc cat gaa gcc    3157
Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala
            975                 980                 985


gga ttg gag cct gca aac ctc gga agt ctg tgg ctg ctc agc ctg gtg    3205
Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val
990                 995                 1000                1005


tat tgg tgt tac agc cag aaa ctt tgg gaa ttc tct tgt tagttggtta    3254
Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys
                1010                1015


gttttactgt aattttctat aaagaattca tatcatctgt taatggcgac agtttttgtt 3314
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tcttcctttg aatttttat attctttctt tctctttttt gtttcttctt ctttgagtat 3374

tttgtaatct tactgggagg gctaaagcgt cttctatcat atcgaattgg gacaatgata 3434

gaagacaatc tttgtttgt cactctaaag aaattattgt aagattttat catcaggtat 3494

gacatttaca ccattgatgt aggcttttta aaaaatatat ccagcctgta ttgggttaag 3554

atgattcttt tctgatcctg atttcctagg agttggtttt tttttttta aagcataaat 3614

aaatttaatt gcatcag   3631

<210> 180

<211> 1018

<212> PRT

<213> Homo sapiens

<400> 180

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu Tyr Lys Tyr

1   5   10   15

Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr Arg Cys Val

            20   25   30

Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser Glu Val Gln

            35   40   45

Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg Lys Thr Val
      50   55   60

Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile Thr Ser Tyr
65   70   75   80

Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys Ile Ile Pro
          85   90   95

Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val Ile Leu Ala
          100   105   110

Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala Val Asn Glu
          115   120   125

Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu Ser Ile Ala
          130   135   140

Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile Val Val Pro
145   150   155   160

Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr Thr Leu Glu
          165   170   175

Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val Thr Trp Lys
          180   185   190

Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe Gly Arg Arg
          195   200   205

Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro Tyr Val Cys
   210   215   220

Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg Ala Thr Ala
225   230   235   240

Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu Pro Glu Ser
         245   250   255

Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly Cys Gln Ala
         260   265   270

Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp Ala Ile Ser
         275   280   285

Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala Ser Gly Gly
   290   295   300

Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile Phe Gln Cys
305   310   315   320

Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr Tyr Leu Asp
         325   330   335

Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val Asp Thr Thr
         340   345   350

Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val Ser Gly Ala

```
                355                    360                        365

Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile Leu Ala Ser
      370                    375                    380

Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser Gly Gly Leu
385                    390                    395                    400

Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr Thr Cys Tyr
                405                    410                    415

Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr Leu Thr Val
                420                    425                    430

Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His Val Val Ile
                435                    440                    445

Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His Asp Pro Arg
      450                    455                    460

Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala Leu Thr Pro
465                    470                    475                    480

Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser Leu Leu Ile
                485                    490                    495

Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys Glu Ile Val
      500                    505                    510
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Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu Val Ile Glu
         515   520   525

Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His
         530   535   540

Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser
545   550   555   560

Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp
         565   570   575

Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val
         580   585   590

Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val
         595   600   605

Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met
         610   615   620

Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser
625   630   635   640

Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu
         645   650   655

Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu
         660   665   670

Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu
        675   680   685

Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu
        690   695   700

Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg
705   710   715   720

Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln
          725   730   735

Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp
          740   745   750

Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys
          755   760   765

Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr
          770   775   780

Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu
785   790   795   800

Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro
          805   810   815

Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp

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                    820                825                830

Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr
        835                840                845

Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile
        850                855                860

Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg
865                870                875                880

Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly
                885                890                895

Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala
                900                905                910

Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro
        915                920                925

Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser
        930                935                940

Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr
945                950                955                960

Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val
                965                970                975
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Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu
        980   985   990

Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys
        995   1000   1005

Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys
    1010   1015

<210> 181

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 181

cttctgctct aaaagctgcg   20

<210> 182

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

<400> 182

cgacctgcag ctcgagcaca   20